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James Martinell
Primary Examiner 1631

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OM nucleic - nucleic search, using sw model

Run on: November 29, 2003, 17:02:55 ; Search time 106 Seconds
(without alignments)
6891.406 Million cell updates/sec

Title: US-09-700-696C-1
Perfect score: 1655
Sequence: 1 gtgaataaagaatatagatat.....ataaaaaaaaaaaaaaaaaa 1655

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	70	4.2	7218	1	US-08-232-463-14
2	48	2.9	2277	1	US-08-676-967-2
3	48	2.9	2277	1	US-08-676-974-2
4	48	2.9	2277	2	US-09-098-487-2
5	42.2	2.5	2621	2	US-08-553-619B-8
6	39.6	2.4	696	3	US-09-461-697-193
7	39.6	2.4	699	3	US-09-461-697-191
8	39.6	2.4	717	3	US-09-461-697-189
9	39.6	2.4	774	3	US-09-461-697-187
10	38.6	2.4	819	3	US-09-461-697-185
11	39.6	2.4	1869	3	US-09-461-697-184
12	39.2	2.4	719	3	US-08-714-918-11
13	39.2	2.4	719	3	US-09-265-315-11
14	39.2	2.4	719	3	US-09-265-315-11
15	39.2	2.4	719	3	US-09-266-417-11
16	39.2	2.4	1850	3	US-08-617-860B-32
17	39.2	2.4	2447	2	US-09-014-963-14
18	39.2	2.4	4098	2	US-08-605-106-4
19	38.6	2.3	1605	4	US-09-369-247-18
20	38	2.3	273	4	US-09-134-001C-132
21	38	2.3	2007	2	US-08-743-637B-169
22	38	2.3	2007	3	US-08-526-840B-169
23	38	2.3	2028	4	US-09-134-001C-1710
24	38	2.3	2422	1	US-07-867-106-5
25	38	2.3	3138	1	US-07-867-106-4
26	38	2.3	5852	1	US-07-867-106-2
C 27	37.8	2.3	1830121	4	US-09-557-884-1

C	28	37.8	2.3	1830121	4	US-09-643-990A-1	Sequence 1, Appli
29	37.6	2.3	1293	4	US-09-370-838-219	Sequence 219, App	
30	37.4	2.3	3527	4	US-08-909-965C-7	Sequence 7, Appli	
31	37.2	2.2	1474	3	US-08-821-994-64	Sequence 64, Appli	
32	36.8	2.2	1038	4	US-09-560-419-4	Sequence 4, Appli	
33	36.8	2.2	2673	4	US-09-336-447A-12	Sequence 12, Appli	
34	36.4	2.2	1134	4	US-09-328-352-3017	Sequence 3017, Ap	
35	36.4	2.2	4285	4	US-09-410-464-1	Sequence 1, Appli	
36	36.4	2.2	1664976	4	US-08-916-421B-1	Sequence 1, Appli	
37	36.2	2.2	681	4	PCT-US95-13658-3	Sequence 2725, Ap	
38	36.2	2.2	870	5	US-08-646-301A-1	Sequence 3, Appli	
39	36.2	2.2	11288	3	US-08-481-968A-4	Sequence 1, Appli	
40	36.2	2.2	11288	4	US-08-154-712B-4	Sequence 4, Appli	
41	36.2	2.2	11288	4	US-08-154-712B-4	Sequence 4, Appli	
42	36.2	2.2	15056	4	US-09-474-699-10	Sequence 10, Appli	
43	36.2	2.2	30549	4	US-09-134-001C-322	Sequence 322, App	
44	36.2	2.2	1664976	4	US-08-916-421B-1	Sequence 1, Appli	
C	44	36	2.2	1219	4	US-08-195-705-1	Sequence 1, Appli
C	45	36	2.2	1219	4	US-08-195-705-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-232-463-14/C
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 INMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
US-08-232-463-14

Query Match 4.2%; Score 70; DB 1; Length 7218;


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Db 394 ACNGTNTTYGNCARTTYGGGNCNGTNTYNGARGTNAAYATHCCNMGNNAARCCNGAYGN 453
QY 466 GATATATCTCTTTTCAGTGGGACGCCCAACCTTTTAAGGACATTCCTGGTAAAGAGAA 525
Db 454 AARATGNGGNTT---YGGNTTYGTNCARTTYAARAYVYTYNGARCGNNGNAARGCN 510
QY 526 GCTACTGCTGCTAGACGAGCAAGATATTCACAAAGGTTTTCAGAGGCCCAAGTGAA 585
Db 511 YTNAARGGNATGAAYATGAARGARATHAARGGNMGNACNGTNGTNGAYTGGGNGTGN 570
QY 586 GCTGAGAGTACTCATCTTGACACAAAGAGCCAGGTTATAATGAGATCCAGAGAGAA 645
Db 571 GCAARGATYAARTYAARGAYACNARWNGTNGWNCNATHGGNGARGARARWNCAY 630
QY 646 GAAATATGTTGGAAATACCAATGGGATGAACTCGAAGAGAGCAGATGCTGTT 705
Db 631 GARWSNAARCAFCARGARWSNGTNAARAARAARGGNMGNARGARGAYATGGARGAR 690
QY 706 GATGTCAGCTTTGAGAGGCGACGACGATATCATGCGGTAGTACCAATTTTAAGGCTC 765
Db 691 GARGARAAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAYGAY 750
QY 766 CTGGAAGAGAGAGAAACAGAGTGGATGCTGCGAGCAGCAAAATGCTCACCAAGGAGGTT 825
Db 751 GAYGARGARGARGARAYATHGARWSNARGTNAACNARCCNGTNCARATHCARARWGN 810
QY 826 GATGTTCAATTCCTCTGACCTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 885
Db 811 GCNGTNAARWNGCNCNGCNCNGCNCNARWSNNGAYCAYWSNNGARGARGAYWSNGAYTN 870
QY 886 GCTGAAGTACCAACTATATGAATCTCTAAATGCGCAAGGCGAGTACCAGAGGCT 945
Db 871 GARGARWSNGAYWSNATHGAYGAYGNGARGARYTNGCNCARWSNGAYACNWSNACNGAR 930
QY 946 GTAGATCAATCTTAATAGGACCAAGCAACCTTAATGAAAGAGAGAGAGAGAGAGAG 1005
Db 931 GARGARGARGAYARCCNGTNCARGTNSWNAAYABARAARMGNAARYTNCNWSNGAY 990
QY 1006 GGCAG 1010
Db 991 GTNAA 995
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RESULT 5

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US-08-553-619B-8
; Sequence 8, Application US/08553619B
; Patent No. 5919705
; GENERAL INFORMATION:
; APPLICANT: DeHaan, Petrus T.
; TITLE OF INVENTION: Virus Resistant Plants
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 5919705artis Crop Protection
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,619B
; FILING DATE: December 1, 1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Marcus-Wyner, Lynn
; REGISTRATION NUMBER: 34,869
; REFERENCE/DOCKET NUMBER: 137-1082/PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/354-3588

; TELEFAX: 415/857-1125
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2621 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; ORIGINAL SOURCE:
; ORGANISM: Chimeric tomato spotted wilt virus S RNA
US-08-553-619B-8

Query Match 2.5%; Score 42.2; DB 2; Length 2621;
Best Local Similarity 54.1%; Pred. No. 0.14; 73; Indels 0; Gaps 0;
Matches 86; Conservative 0; Mismatches 0;

QY 1497 TAAGCAAAAAAATCAATACAGATCTATGAATAAGTAACTTTGAGTAGGTGTCATTT 1556
Db 667 TATAATATATAAAGTTCTTTAATCTTTATGCTTGTGCTTGTGTTAAATTT 726
QY 1557 AAAATAGTGTGGTGAATGTCAAAATGCTTCTATGTTGTTGCTCTGTAGACATGAAA 1616
Db 727 TAAATAAGTGTGTTTAAATTAAGTTTGTCTTCTGTTGTTGTTTAAATAATAAATAA 786
QY 1617 TAAACAATATCTCTCGATGATAAAAAAATAAAAAA 1655
Db 787 TAACAAAAAACAAGAAACAAAAATAATAATAAATAA 825

RESULT 6
US-09-461-697-193
; Sequence 193, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Purnam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461,697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 193
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-697-193

Query Match 2.4%; Score 39.6; DB 3; Length 696;
Best Local Similarity 43.6%; Pred. No. 0.37;
Matches 177; Conservative 0; Mismatches 229; Indels 0; Gaps 0;

QY 517 AAAGGAGAAAGTACTGTCTCTGACCTAGAGGCAAGATATTCAAAACAGGTTTGACGGC 576
Db 268 AAAGGGAGAGTGGAAAGAGACAAAGATGAAAGGGGAGAGATGGAAGAGAGGAT 327
QY 577 CCAAGTGAAGCTGAGAGTACTCATTTGACACAAAAAAGCCAGGTTTATATGAGATCCCA 636
Db 328 AAAAATGGAATGAGAAAGAGAGATGCAAAAGAGAGAGATGGAAGAGAGAGTGA 387
QY 637 GAGAGAGAGAAATGCTGGAATACCATTTGGAACCTAGGAGTAACTGCGAAGAGGCA 696
Db 388 GACGGAAGAGGAATGGAAGATGGAAGAGAGAGATGGAAGAGAGAGAGAGAGAA 447
QY 697 GATGCTGTTGATGTCAGCTTGTAGAGGCGACAGCATATCATGCTGTTAGTACCAATTT 756
Db 448 GACAGAAAGAGAACAGGAGTGTGGAAGAGAGATGAAGATGGAAGAGAGAGAGATGA 507
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QY 757 AAGGAGCTCCCTGGAAAGAGAGAAACAGAGTGTGCTGGCAGCCCAAAATGCTCACAA 816
Db 508 AAAGAGGGGAAGATGTAAAGTCAAGAAAGATGAAAGAGAGAGAGATGGAAGAA 567
QY 817 GGAAGGTTGAGTTTATTTACCTCTGACCCCTCAAAAGAGAGAAAGAGAGGAGT 876
Db 568 GATGAAGGTTGAAATGAGGAAGAGCTGGAAAGAGAGAAAGATTTAAAGAGAGGAA 627
QY 877 AGTGATGCAGCTGAAAGTACCACTATAATGAAATTCCTAAATG 922
Db 628 GAAGGAAAGAGGAGAGATGAGATCAAGAGAGATGATGGAAGAAAG 673

RESULT 7
US-09-461-697-191
; Sequence 191, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461,697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 191
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-697-191

Query Match 2.4%; Score 39.6; DB 3; Length 699;
Best Local Similarity 43.6%; Pred. No. 0.37;
Matches 177; Conservative 0; Mismatches 229; Indels 0; Gaps 0;
QY 517 AAAGGAGAGCTACTGTCTGCTAGCCTAGAGGCAAGATATTCACACAGGCTTTGCAGGC 576
Db 271 AAAGGGGAAGCTGGAAAGAGAGCAAAAGATGAAAGAGGGGAGAGATGGAAGAGAGAT 330
QY 577 CCAAGTGAAGCTGAGAGTACTCTTGCACACAAAAAGCCAGCTTATATGAGATCCCA 636
Db 331 AAAAATGGAATGAGAAAGGAGAGATGCAAAAGAGAAAGAGATGGAAGAAAGGTGAA 390
QY 637 GAGAGAGAGAAATGTTGAAATACCATTTGAACTAGGGATGAACTGCGAAAGAGGCA 696
Db 391 GACGAAAGGAAATGAGAGAGATGGAAAGAGAGAGAGAGATGAAAGAGAGAGAA 450
QY 697 GATGCTGTTGATGTCAGCTTGTAGAGGCGAGCAACATATCATGCTGGTAGTACCAATTTT 756
Db 451 GACAGAAAGAGAAACAGGAGTTGGAAAGAGAGATGAAGATGGAAGAGAGAGAGATGAA 510
QY 757 AAGGAGCTCCCTGGAAGAGAGAGAAACAGAGTGTGCTGGCAGCCCAAAATGCTCACAA 816
Db 511 AAAGGGGGAAGATGTAAAGTCAAGAGATGAAAGAGAGAGAGATGGAAGAAAGAA 570
QY 817 GGAAGGTTGAGTTTCAATTCCTCTGACCCCTCAAAAGAGAGAAAGAGAGGAGT 876
Db 571 GATGAAGTGAATGAGGAAGAGCTGGAAAGAGAGAAAGATTTAAAGAGAGAGAA 630
QY 877 AGTGATGCAGCTGAAAGTACCACTATAATGAAATTCCTAAATG 922
Db 631 GAAGGAAAGAGGAGAGATGAGATCAAGAGAGATGATGGAAGAAAG 676

RESULT 8
US-09-461-697-189
; Sequence 189, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461,697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 189
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-697-189

Query Match 2.4%; Score 39.6; DB 3; Length 717;
Best Local Similarity 43.6%; Pred. No. 0.37;
Matches 177; Conservative 0; Mismatches 229; Indels 0; Gaps 0;
QY 517 AAAGGAGAGCTACTGTCTGCTAGCCTAGAGGCAAGATATTCACACAGGCTTTGCAGGC 576
Db 289 AAAGGGGAAGCTGGAAAGAGAGCAAAAGATGAAAGAGGGGAGAGATGGAAGAGAGAT 348
QY 577 CCAAGTGAAGCTGAGAGTACTCTTGCACACAAAAAGCCAGCTTATATGAGATCCCA 636
Db 349 AAAAATGGAATGAGAAAGGAGAGATGCAAAAGAGAAAGAGATGGAAGAAAGGTGAA 408
QY 637 GAGAGAGAGAAATGTTGAAATACCATTTGAACTAGGGATGAACTGCGAAAGAGGCA 696
Db 409 GACGAAAGGAAATGAGAGAGATGGAAAGAGAGAGAGAGATGAAAGAGAGAGAGAA 468
QY 697 GATGCTGTTGATGTCAGCTTGTAGAGGCGAGCAACATATCATGCTGGTAGTACCAATTTT 756
Db 469 GACAGAAAGAGAAACAGGAGTTGGAAAGAGAGATGAAGATGGAAGAGAGAGAGATGAA 528
QY 757 AAGGAGCTCCCTGGAAGAGAGAGAAACAGAGTGTGCTGGCAGCCCAAAATGCTCACAA 816
Db 529 AAAGAGGGGGAAGATGTAAAGTCAAGAGATGAAAGAGAGAGAGAGATGGAAGAGAA 588
QY 817 GGAAGGTTGAGTTTCAATTCCTCTGACCCCTCAAAAGAGAGAAAGAGAGGAGT 876
Db 589 GATGAAGTGAATGAGGAAGAGCTGGAAAGAGAGAGAGATTTAAAGAGAGAGGAA 648
QY 877 AGTGATGCAGCTGAAAGTACCACTATAATGAAATTCCTAAATG 922
Db 649 GAAGGAAAGAGGAGAGATGAGATCAAGAGAGATGATGGAAGAAAG 694

RESULT 9
US-09-461-697-187
; Sequence 187, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING

```
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461,697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-697-187

Query Match      2.4%; Score 39.6; DB 3; Length 774;
Best Local Similarity 43.6%; Pred. No. 0.39;
Matches 177; Conservative 0; Mismatches 229; Indels 0; Gaps 0;

QY 517 AAAGGAGAACTACTGCTCCTGACCTAGAGGCAAGATATTCACACAGGGTTTCAGGC 576
D 346 AAAGGGGAAGCTGGAAAGAGACAAAGATGAAAGAGGGGAGAGATGGAAAGAGAT 405
QY 577 CCAAGTGAAGCTGAGAGTACTCATCTTGACACAAAAAGCCAGGTATTAATGAGATCCCA 636
D 406 AAAAAATGGAATGAGAAAGAGAGATGCAAAAAGAGAAAGATGGAAGAAAGGTGAA 465
QY 637 GAGAGAGAGAAATGTTGGAATACCACTTGAAGTGGAGTGAATGCGGAAAGAGCA 696
D 466 GACGGAAGGAAATGAGAGAGATGGAAGAGAGAAAGAGAGAGATGAAAAAGGGAAGAA 525
QY 697 GATCCTGTGATGTCAGCTTGTAGAGGCGAGCAACGATATCATGGGTAGTACCAATTTT 756
D 526 GACGAAAGAAACAGAGATTGGAAGAGATGAAGTGAAGAGAGAGAGAGAGATGAA 585
QY 757 AAGGAGCTCCTGGAAGAGAGAGAAACAGATGATGCTGCGAGCCAAATGCTCACCAA 816
D 586 AAAGGAGGAAAGATGTAAGAGTCAAGAGATGAAGAGAGAGAGAGAGATGGAAGAA 645
QY 817 GGGAGGTTGAGTTTCAATACCTCCCTGACCCCTCAAGAGAGAGAGAGAGAGAGAGT 876
D 646 GATGAAGTGGAAATGAGGAGAGAGTGGAAAGAGAGAGAGAGATTTTAAAGAGAGAGAA 705
QY 877 AGTGATGAGCTGAAGATGACCACTATATGAATGAAATTCCTAAAAATG 922
D 706 GAAGGAAAGAGGAGATGAGATCAAGAGATGATGAAAAAAG 751

RESULT 10
US-09-461-697-185
; Sequence 185, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461,697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 185
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-697-185

Query Match      2.4%; Score 39.6; DB 3; Length 819;
Best Local Similarity 43.6%; Pred. No. 0.4;
Matches 177; Conservative 0; Mismatches 229; Indels 0; Gaps 0;

QY 517 AAAGGAGAACTACTGCTCCTGACCTAGAGGCAAGATATTCACACAGGGTTTCAGGC 576
D 470 AAAGGGGAAGCTGGAAAGAGACAAAGATGAAAGAGGGGAGAGATGGAAGAAAGAGAT 529
QY 577 CCAAGTGAAGCTGAGAGTACTCATCTTGACACAAAAAGCCAGGTATTAATGAGATCCCA 636
D 530 AAAAAATGGAATGAGAAAGAGAGATGCAAAAAGAGAAAGATGGAAGAAAGGTGAA 589
QY 637 GAGAGAGAGAAATGTTGGAATACCACTTGAAGTGGAGTGAATGCGGAAAGAGCA 696
D 590 GACGGAAGGAAATGAGAGAGATGGAAGAGAGAGAGAGAGATGAAAAAGAGAGAA 649

RESULT 11
US-09-461-697-184
; Sequence 184, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461,697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 184
; LENGTH: 1669
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-697-184

Query Match      2.4%; Score 39.6; DB 3; Length 1669;
Best Local Similarity 43.6%; Pred. No. 0.55;
Matches 177; Conservative 0; Mismatches 229; Indels 0; Gaps 0;

QY 517 AAAGGAGAACTACTGCTCCTGACCTAGAGGCAAGATATTCACACAGGGTTTCAGGC 576
D 470 AAAGGGGAAGCTGGAAAGAGACAAAGATGAAAGAGGGGAGAGATGGAAGAAAGAGAT 529
QY 577 CCAAGTGAAGCTGAGAGTACTCATCTTGACACAAAAAGCCAGGTATTAATGAGATCCCA 636
D 530 AAAAAATGGAATGAGAAAGAGAGATGCAAAAAGAGAAAGATGGAAGAAAGGTGAA 589
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QY 697 GATGCTGTTGATGTCAGCCTTGTAGAGGGCAGCAACGATATCATGGTAGTACCAATTTT 756
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QY 757 AAGGAGCTCCCTGGAAAGAGAGAAACAGAGTGGATGCTGGCAGCCAAATGCTCACCAA 816
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Db 710 AAAGAGGGAAAGAGATCTAAAGTCAAGAGAGATGAAAAGAGAGAGAGATGGAAGAA 769
QY 817 GGAAGGTTGAGTTTCATTACCTCTGACCCCTCAAAGAGAGAAAAGAAAGAGGAGT 876
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Db 770 GATGAGGTGGAATGAGGAAGAGCTGGAAAAGAGAGAAAGAGATTTAAAGAGAGAGAA 829
QY 877 AGTGATGACGCTGAAAGTACCACTATAATGAAATTCCTAAATAATG 922
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Db 830 GAAGGAAAAGAGAGATGAGATCAAGAGAGATGAGGAAAAAAG 875

RESULT 12
US-08-714-918-11/c
; Sequence 11, Application US/08714918
; Patent No. 6037123

GENERAL INFORMATION:

; APPLICANT: Benton, Bret
; APPLICANT: Lee, Ving
; APPLICANT: Malouin, Francois
; APPLICANT: Martin, Patrick K.
; APPLICANT: Schmid, Molly B.
; APPLICANT: Sun, Dongxu

; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
; TITLE OF INVENTION: TARGET GENES
; NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/714,918
; FILING DATE: September 13, 1996
; CLASSIFICATION: 424

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/009,102
; FILING DATE: December 22, 1995
; APPLICATION NUMBER: 60/003,798
; FILING DATE: September 15, 1995

ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 222/005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 719 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-714-918-11

Query Match

Best Local Similarity 2.4%; Score 39.2; DB 3; Length 719;
Matches 74; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

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Db 378 ACTATGTTTCATTCACAAATTAATATGCAATATGAATAGTCATAATTTGCTTTTG 319
QY 1549 TGTCAATTTAAATAATAGTTGGTGAATGTCACAAATGCTTCTATGTTGTTGCTCTGTAGA 1608
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Db 318 GAGTATAAAAAGCACCTTGTGCAAAAAACACAGTGCCTTTAACTTTAATTTATTGTTCACT 259
QY 1609 CATGAAAAATAA 1620
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Db 258 AGTTTGAATCAA 247

RESULT 13

US-09-265-315-11/c
; Sequence 11, Application US/09265315
; Patent No. 6187541

GENERAL INFORMATION:

; APPLICANT: Benton, Bret
; APPLICANT: Lee, Ving J.
; APPLICANT: Malouin, Francois
; APPLICANT: Martin, Patrick K.
; APPLICANT: Schmid, Molly B.
; APPLICANT: Sun, Dongxu

; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
; NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/265,315
; FILING DATE: March 9, 1999
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/714,918
; FILING DATE: September 13, 1996
; APPLICATION NUMBER: 60/009,102
; FILING DATE: December 22, 1995
; APPLICATION NUMBER: 60/003,798
; FILING DATE: September 15, 1995

ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 240/247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 719 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-09-265-315-11

Query Match

Best Local Similarity 2.4%; Score 39.2; DB 3; Length 719;
Matches 74; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

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Qy	1549	TGTCATTTAAAAATAGTTGGTGAATGTCACAAATGCCCTTCTATGTTGTTGCTCTGTAGA	1608
Db	318	GAGTATAAAAGCACTTGTGCAAAACACAAAGTGTCTTAAACTTAATTATTGTTCACT	259
Qy	1609	CATGAAAATAAA	1620
Db	258	AGTTGAATCAA	247

Search completed: November 29, 2003, 18:15:24
Job time : 110 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 29, 2003, 18:13:30 ; Search time 535 Seconds
(without alignments)
10191.985 Million cell updates/sec

Title: US-09-700-696C-1
Perfect score: 1655
Sequence: 1 gtgaataagaatatagatat.....ataaaaaaaaaaaaaaaaaa 1655

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2190069 seqs, 1647345023 residues

Total number of hits satisfying chosen parameters: 4380138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1638	99.0	1876	12	US-09-794-422-33 Sequence 33, Appl
2	1638	99.0	1969	12	US-09-794-422-45 Sequence 45, Appl
3	1638	99.0	2019	12	US-09-794-422-5 Sequence 5, Appl
4	1638	99.0	2112	12	US-09-794-422-7 Sequence 7, Appl
5	1369	82.7	1662	12	US-10-311-840-3 Sequence 3, Appl
6	1289	77.9	1575	12	US-10-311-840-2 Sequence 2, Appl
7	514.8	31.1	1655	12	US-09-794-422-1 Sequence 1, Appl
8	485.2	29.3	1682	12	US-09-794-422-3 Sequence 3, Appl
9	60	3.6	60	12	US-09-308-975-16013 Sequence 16013, A
C 10	47.6	2.9	3673778	12	US-10-312-841-1 Sequence 1, Appl
C 11	46.8	2.8	345	12	US-09-814-353-5466 Sequence 5466, Ap
C 12	46.8	2.8	345	12	US-09-814-353-11753 Sequence 11753, A
C 13	46.6	2.8	2836	12	US-10-032-585-6930 Sequence 6930, Ap
C 14	45.8	2.8	2000	10	US-09-887-576-831 Sequence 831, Appl
C 15	44.8	2.7	3673778	12	US-10-312-841-2 Sequence 2, Appl
C 16	44.6	2.7	349	12	US-09-814-353-18039 Sequence 18039, A

17	44.6	2.7	637	12	US-10-027-632-244151	Sequence 244151,
18	44.6	2.7	637	12	US-10-027-632-244152	Sequence 244152,
19	44.6	2.7	637	13	US-10-027-632-244151	Sequence 244151,
20	44.6	2.7	637	13	US-10-027-632-244152	Sequence 244152,
C 21	44.4	2.7	5218	12	US-10-311-455-1239	Sequence 1239, Ap
C 22	44.4	2.7	14006	12	US-10-311-455-1931	Sequence 1931, Ap
C 23	44.2	2.7	403	12	US-09-814-353-17949	Sequence 17949, A
C 24	44.2	2.7	8530	12	US-10-311-455-1727	Sequence 1727, Ap
C 25	44.2	2.7	21537	12	US-10-311-455-1971	Sequence 1971, Ap
C 26	44	2.7	6155	12	US-10-340-453-235	Sequence 235, App
C 27	44	2.7	9997	12	US-10-311-455-342	Sequence 342, App
C 28	44	2.7	9997	12	US-10-240-485-38	Sequence 38, Appl
C 29	43.6	2.6	341	10	US-09-960-352-12302	Sequence 12302, A
C 30	43.4	2.6	631	12	US-09-814-353-5993	Sequence 5993, Ap
C 31	43.4	2.6	631	12	US-09-814-353-12272	Sequence 12272, A
C 32	43.2	2.6	7634	12	US-10-311-455-2103	Sequence 2103, Ap
C 33	43.2	2.6	8962	12	US-10-311-455-2103	Sequence 659, App
C 34	43	2.6	65	12	US-09-908-975-111	Sequence 111, App
C 35	43	2.6	6587	12	US-10-311-455-358	Sequence 358, App
C 36	43	2.6	10377	12	US-10-311-455-2193	Sequence 2193, Ap
C 37	42.8	2.6	5204	12	US-10-311-455-872	Sequence 872, App
C 38	42.8	2.6	5369	12	US-10-311-455-525	Sequence 525, App
C 39	42.8	2.6	7703	12	US-10-311-455-1408	Sequence 1408, Ap
C 40	42.8	2.6	11729	12	US-10-311-455-868	Sequence 868, App
C 41	42.8	2.6	32195	14	US-10-102-627-92	Sequence 92, Appl
C 42	42.6	2.6	747	12	US-10-140-472-212	Sequence 212, App
C 43	42.6	2.6	747	12	US-10-141-761-212	Sequence 212, App
C 44	42.6	2.6	747	12	US-10-142-885-212	Sequence 212, App
C 45	42.6	2.6	747	12	US-10-158-790-212	Sequence 212, App

ALIGNMENTS

RESULT 1

US-09-794-422-33
; Sequence 33, Application US/09794422
; Publication No. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-794-422-33

Query Match 99.0%; Score 1638; DB 12; Length 1876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1638; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2	TGAATAAAGAAATAGTATCAGTAACAAGAGAAATCTCACAATGGCTGAGGATGTCAA	61
Db	239	TGAATAAAGAAATAGTATCAGTAACAAGAGAAATCTCACAATGGCTGAGGATGTCAA	298
Qy	62	TTTATCTTAAGTCACTGGGAATAAGGGTTTGAGATGAGATGATCTATCAGCAAAAC	121
Db	299	TTTATCTTAAGTCACTGGGAATAAGGGTTTGAGATGAGATGATCTATCAGCAAAAC	358
Qy	122	TACATGACCAAGAAGATATGGCGAGCTCTCATCGAATAACATGCACATATATGG	181

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RESULT 2

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US-09-794-422-45
? Sequence 45, Application US/09794422
? Publication No. US20030166239A1
? GENERAL INFORMATION:
?
? APPLICANT: Brown, Thomas A.
? APPLICANT: De Wet, Jeffrey R.
? APPLICANT: Gowen, Lori C.
? APPLICANT: Hanes, Lynn M.
? TITLE OF INVENTION: Mammalian Osteoregulins
?
? FILE REFERENCE: PCl0445
? CURRENT APPLICATION NUMBER: US/09/794,422
? CURRENT FILING DATE: 2001-02-27
? PRIOR APPLICATION NUMBER: 60/185,617
? PRIOR FILING DATE: 2000-02-29
? PRIOR APPLICATION NUMBER: 60/234,500
? PRIOR FILING DATE: 2000-09-22
? NUMBER OF SEQ ID NOS: 46
? SOFTWARE: PatentIn ver. 2.0
?
? SEQ ID NO 45
? LENGTH: 1969
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-794-422-45

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Query Match	99.0%;	Score 1638;	DB 12;	Length 1969;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1638.	Conservative	0.	Mismatches	0.
			Indels	0.
			Gaps	0.

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Qy	62	TTTATCCTAAGTCAACTGGGAATAAAGGTTTGAGGATGGAGATGATGCTTATCAGCAAAAC	121
Db	392	TTTATCCTAAGTCAACTGGGAATAAAGGTTTGAGGATGGAGATGATGCTTATCAGCAAAAC	451
Qy	122	TACATGACCAAGAAGAAATATGGCGACCTCTCATCAGAAATAACATGCAACATATAATGG	181
Db	452	TACATGACCAAGAAGAAATATGGCGACCTCTCATCAGAAATAACATGCAACATATAATGG	511
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Qy 662 CCATTGGAACTAGGATGAAATCGCGAAAGAGGAGATCTGTTGATGTCAGCTTTGAG 721
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Qy 722 AGGGCAGCAACGATATCATGGGTAGTACCAATTTAAAGAGTCCCTGGAAAGAGGAA 781
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Qy 782 ACAGATGGATCTCGCAGCCAAATGCTCCACAGGAGAGTTCAGTTTCATTAACCTC 841
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Db 1172 CTGCACTCTCAAAAGAGAGAGAGAGAGAGGAGTGTGATGAGCTGAAAGTACCAACT 1231
Qy 902 ATAATGAATTCCTAAATGCGAAGGAGGAGTACGAGAGAGGAGTGTGATGATTCATATA 961
Db 1232 ATAATGAATTCCTAAATGCGAAGGAGGAGTACGAGAGAGGAGTGTGATGATTCATATA 1291
Qy 962 GGAAACCAAGCACTTAAATGAAACAAAGGTTTCTAGTAAAGGCAAAAGTCAAGGCC 1021
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RESULT 3

US-09-794-422-5
; Sequence 5, Application US/09794422
; Publication NO. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PCI0445
; CURRENT APPLICATION NUMBER: US/09/794,422
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-794-422-5

Query Match 99.0%; Score 1638; DB 12; Length 2019;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1638; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 122 TACATGACCAAGAGAAATATGGCGAGCTCTCATCAGAAATAACATGCAACATATAATGG 181
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QY 662 CCATTGGAACTAGGGATGAACTGCGAAAGAGCGAGATGCTGTGATGTCAGCCTTGTAG 721
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QY 1022 TGCCCATCTCTCTGCTGCTTGTATGATAATGAAATCAAAAACGAAATGGATTCCTTTAATG 1081
Db 1495 TGCCCATCTCTCTGCTGCTTGTATGATAATGAAATCAAAAACGAAATGGATTCCTTTAATG 1554
QY 1082 GCCCAGTCATGAGATATAATAACATGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1141
Db 1555 GCCCAGTCATGAGATATAATAACATGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1614
QY 1142 AAAATAATCTACAGGAATAAGGATATGCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1201
Db 1615 AAAATAATCTACAGGAATAAGGATATGCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1674
QY 1202 CCATTTCAACAGGAGGTTAGTTCCTGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1261
Db 1675 CCATTTCAACAGGAGGTTAGTTCCTGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1734
QY 1262 GTGGCAGTTTCAAGTGAAGCGATGCTGACTAGTCCACAGAGAGAGTCCCAAGCGGGTGACA 1321
Db 1735 GTGGCAGTTTCAAGTGAAGCGATGCTGACTAGTCCACAGAGAGAGTCCCAAGCGGGTGACA 1794
QY 1322 GTCTGAAGACCTCGTCACTGTGAGTTGATGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1381
Db 1795 GTCTGAAGACCTCGTCACTGTGAGTTGATGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1854
QY 1382 GTGAAGAGAGGATAGAGTGAAGAACTGTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1441
Db 1855 GTGAAGAGAGGATAGAGTGAAGAACTGTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1914

QY 1442 TTTTGTCTATCTTAATAGTCAAGTATATAAATTTCTATTAAAGCTATATAATGTTTTAAGC 1501
Db 1915 TTTTGTCTATCTTAATAGTCAAGTATATAAATTTCTATTAAAGCTATATAATGTTTTAAGC 1974
QY 1502 AAAAAAATCAATACAGATCTATGAAATAGGTAAATTTGAGTAGGTGTCAATTTAAAAA 1561
Db 1975 AAAAAAATCAATACAGATCTATGAATAGGTAAATTTGAGTAGGTGTCAATTTAAAAA 2034
QY 1562 TAGTTGGTGAATGTCAAAATGCTTCTATGTTGTTTGTCTGTGACATGAAAAATAAAC 1621
Db 2035 TAGTTGGTGAATGTCAAAATGCTTCTATGTTGTTTGTCTGTGACATGAAAAATAAAC 2094
QY 1622 AATATCTCTCGATGATAA 1639
Db 2095 AATATCTCTCGATGATAA 2112

RESULT 5

US-10-311-840-3
; Sequence 3, Application US/10311840
; Publication No. US2003017580A1
; GENERAL INFORMATION:
; APPLICANT: KUROKAWA, Tomofumi
; APPLICANT: YAMADA, Takao
; APPLICANT: MORIMOTO, Shigeto
; TITLE OF INVENTION: No. US2003017580A1 Protein and its DNA
; FILE REFERENCE: 2738USOP
; CURRENT APPLICATION NUMBER: US/10/311,840
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: PCT/JP01/05263
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: JP 2000-191088
; PRIOR FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 3
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Human
US-10-311-840-3

Query Match 82.7%; Score 1369; DB 12; Length 1662;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGAATAAAGAATATAGTATCAGTAAACAAAGAGAAATCTCAATGCGCTGAGGATGTCAA 61
Db 294 TGAATAAAGAATATAGTATCAGTAAACAAAGAGAAATCTCAATGCGCTGAGGATGTCAA 353
QY 62 TTTATCTTAAGTCACTGGGAATAAGGTTTGGAGATGGAGATGCTATCAGCAAC 121
Db 354 TTTATCTTAAGTCACTGGGAATAAGGTTTGGAGATGGAGATGCTATCAGCAAC 413
QY 122 TACATGACCACAAAGAATATGCGCAGCTCTCATCAGAAATAACATGCAACATATAATGG 181
Db 414 TACATGACCACAAAGAATATGCGCAGCTCTCATCAGAAATAACATGCAACATATAATGG 473
QY 182 GGCAGTGTACTGCGATTTAAATCTCTGGGGAAGAAAACAAAGAGAACACACCTTAGAATG 241
Db 474 GGCAGTGTACTGCGATTTAAATCTCTGGGGAAGAAAACAAAGAGAACACACCTTAGAATG 533
QY 242 TTCTAAACATATCCCGCAAGTATGAATTTATGCTTAAAGCACTCTGAGGATATAAAGA 301
Db 534 TTCTAAACATATCCCGCAAGTATGAATTTATGCTTAAAGCACTCTGAGGATATAAAGA 593
QY 302 AGCCTCAAAGAGATTTCCCAAGCCGAGAAAGTCCAGTAAAGAAACCAACCCATCGTA 361
Db 594 AGCCTCAAAGAGATTTCCCAAGCCGAGAAAGTCCAGTAAAGAAACCAACCCATCGTA 653
QY 362 TTCAAACAACATTTGACTACCTTAAACATCTCTCAAAAGTCAAAAAATCCCCAGTGATT 421
Db 654 TTCAAACAACATTTGACTACCTTAAACATCTCTCAAAAGTCAAAAAATCCCCAGTGATT 713

```
QY 422 TTGAAGCAGCGGTTATACAGATCTTCAAGAGAGGGGACAAATGATATATCTCCTTTCA 481
Db 714 TTGAAGCAGCGGTTATACAGATCTTCAAGAGAGGGGACAAATGATATATCTCCTTTCA 773
QY 482 GTGGGACGCGCAACCTTTTAAAGACATCTCTGTAAAGAGAGACTACTGTGCTCTGACC 541
Db 774 GTGGGACGCGCAACCTTTTAAAGACATCTCTGTAAAGAGAGACTACTGTGCTCTGACC 833
QY 542 TAGAAGGCAAAAGATATTTCAAAAGGGTTTTCAGGCCCAAGTGAAGCTGAGAGTACTCATC 601
Db 834 TAGAAGGCAAAAGATATTTCAAAAGGGTTTTCAGGCCCAAGTGAAGCTGAGAGTACTCATC 893
QY 602 TTGACACAAAAAAGCCAGGTTTATAATCAGATCCAGAGAGAGAGAAATGGTGGAAATA 661
Db 894 TTGACACAAAAAAGCCAGGTTTATAATGAGATCCAGAGAGAGAGAAATGGTGGAAATA 933
QY 662 CCATTGGAATCTAGGATGAAATGCGGAAAGAGGAGATGCTGTGATGTGAGCTTGTAG 721
Db 954 CCATTGGAATCTAGGATGAAATGCGGAAAGAGGAGATGCTGTGATGTGAGCTTGTAG 1013
QY 722 AGGCGACACGATATCATGGTAGTACCAATTTTAAAGGAGCTCCCTGGAGAGAGGAA 781
Db 1014 AGGCGACACGATATCATGGTAGTACCAATTTTAAAGGAGCTCCCTGGAGAGAGGAA 1073
QY 782 ACAGAGTGGATGCTGGCAGCCAAATGCTCAACCAAGGAAAGGTGAGTTTCATTACCCCTC 841
Db 1074 ACAGAGTGGATGCTGGCAGCCAAATGCTCAACCAAGGAAAGGTGAGTTTCATTACCCCTC 1133
QY 842 CTGCACCTCAAAGAGAAAGAAAGAGCGAGTAGTATGAGCTGGAAGTACCAACT 901
Db 1134 CTGCACCTCAAAGAGAAAGAAAGAGCGAGTAGTATGAGCTGGAAGTACCAACT 1193
QY 902 ATATGAAATCTTAAATGCGAAAGCGAGTACCAAGAGGAGTGTAGTCTTAATA 961
Db 1194 ATATGAAATCTTAAATGCGAAAGCGAGTACCAAGAGGAGTGTAGTCTTAATA 1253
QY 962 GGAACCAAGCAACTTAAATGAAAAAAGAGGTTTCTTAGTAAAGGCAAGGTCAGGGCC 1021
Db 1254 GGAACCAAGCAACTTAAATGAAAAAAGAGGTTTCTTAGTAAAGGCAAGGTCAGGGCC 1313
QY 1022 TGCCCATCTCTCTGCTGCTTGAATGAATGAAATCAAAAAAGAAATGATTCCTTTAATG 1081
Db 1314 TGCCCATCTCTCTGCTGCTTGAATGAATGAAATCAAAAAAGAAATGATTCCTTTAATG 1373
QY 1082 GCCCAGTGTAGATATTAACATGCGAGAAATATCATATGATACCCACAGAC 1141
Db 1374 GCCCAGTGTAGATATTAACATGCGAGAAATATCATATGATACCCACAGAC 1433
QY 1142 AAAATTAATCTACACGGAATAAGGGTATGCCAAGGGAAAGGCTCCTGGGGTAGACAAC 1201
Db 1434 AAAATTAATCTACACGGAATAAGGGTATGCCAAGGGAAAGGCTCCTGGGGTAGACAAC 1493
QY 1202 CCATTCCACAGAGGTTTAGTTCCTGAGAGAGGATGACAGTAGTGTGATCTGACA 1261
Db 1494 CCATTCCACAGAGGTTTAGTTCCTGAGAGAGGATGACAGTAGTGTGATCTGACA 1553
QY 1262 GTGCGAGTTCAAGTGAGAGCGATGCTGACTAGTCCACAGAGGTTTCCAGCGGGTGACA 1321
Db 1554 GTGCGAGTTCAAGTGAGAGCGATGCTGACTAGTCCACAGAGGTTTCCAGCGGGTGACA 1613
QY 1322 GTCTGAAGACCTGCTACCTGTGAGTTGATGTAGAGAGGCCACCTGA 1370
Db 1614 GTCTGAAGACCTGCTACCTGTGAGTTGATGTAGAGAGGCCACCTGA 1662
```

RESULT 6

US-10-311-840-2

; Sequence 2, Application US/10311840
; Publication No. US20030175808A1
; GENERAL INFORMATION:
; APPLICANT: KUROKAWA, Tomofumi
; APPLICANT: YAMADA, Takao
; APPLICANT: MORIMOTO, Shigeto

; TITLE OF INVENTION: No. US20030175808A1el Protein and its DNA
; FILE REFERENCE: 2738USOP
; CURRENT APPLICATION NUMBER: US/10/311,840
; PCT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: PCT/JP01/05263
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: JP 2000-191088
; PRIOR FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 2
; LENGTH: 1575
; TYPE: DNA
; ORGANISM: Human
; US-10-311-840-2

Query Match 77.9%; Score 1289; DB 12; Length 1575;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	2	TGAATAAAGATATAGTATCAGTAACAACAGAGATATCTCAATGGCTCGAGGATGCA	61
Db	287	TGAATAAAGATATAGTATCAGTAACAACAGAGATATCTCAATGGCTCGAGGATGCA	346
QY	62	TTTATCCTAAGTCAACTGGGAATAAAGGGTTTGAGGATGAGATGCTATCAGCAAC	121
Db	347	TTTATCCTAAGTCAACTGGGAATAAAGGGTTTGAGGATGAGATGCTATCAGCAAC	406
QY	122	TACATGACCAAGAAATATATGGCGAGCTCTCATCAGAAATAACATCAATATAATGG	181
Db	407	TACATGACCAAGAAATATATGGCGAGCTCTCATCAGAAATAACATCAATATAATGG	466
QY	182	GGCCAGTGTCTGGATTAATACTCTGGGGAAGAAACAAAGAGACACACCTAGGAATG	241
Db	467	GGCCAGTGTCTGGATTAATACTCTGGGGAAGAAACAAAGAGACACACCTAGGAATG	526
QY	242	TTCTAAACATAATCCCAAGCAAGTATGAATATGCTAAAGCACACTCGAAGGATAAAGA	301
Db	527	TTCTAAACATAATCCCAAGCAAGTATGAATATGCTAAAGCACACTCGAAGGATAAAGA	586
QY	302	AGCCTCAAGAGATTTCCAAAGCCAGAAAGTCCAGTAAAGCAAAAGCAACCATCGTA	361
Db	587	AGCCTCAAGAGATTTCCAAAGCCAGAAAGTCCAGTAAAGCAAAAGCAACCATCGTA	646
QY	362	TTCAACACACATGTACTACTTAACATCTCTCAAAAGTCAAAATCCCGCTGATT	421
Db	647	TTCAACACACATGTACTACTTAACATCTCTCAAAAGTCAAAATCCCGCTGATT	706
QY	422	TTCAAGGCGAGCGTTATACAGATCTTCAAGAGAGAGGGGACAATGATATATCTCTTCA	481
Db	707	TTCAAGGCGAGCGTTATACAGATCTTCAAGAGAGAGGGGACAATGATATATCTCTTCA	766
QY	482	GTGGGACGCGCAACCTTTTAAAGACATTTCTGTTAAAGAGAGAGCTTGTGCTGACC	541
Db	767	GTGGGACGCGCAACCTTTTAAAGACATTTCTGTTAAAGAGAGAGCTTGTGCTGACC	826
QY	542	TAGAAGCAAAAGATATTCAAAAGGGTTTTCAGGCCCAAGTGAAGCTGAGAGTACTCATC	601
Db	827	TAGAAGCAAAAGATATTCAAAAGGGTTTTCAGGCCCAAGTGAAGCTGAGAGTACTCATC	886
QY	602	TTGACACAAAAAGCCAGGTTTATAATCAGATCCAGAGAGAGAGAAATGGTGGAAATA	661
Db	887	TTGACACAAAAAGCCAGGTTTATAATCAGATCCAGAGAGAGAGAAATGGTGGAAATA	946
QY	662	CAATTGGAACTAGGATGAAATTCGAAAGAGGCGAGATGCTGTTGATGTGAGCTTGTAG	721
Db	947	CAATTGGAACTAGGATGAAATTCGAAAGAGGCGAGATGCTGTTGATGTGAGCTTGTAG	1006
QY	722	AGGCGAGCAACGATATCATGGGTAGTACCAATTTTAAAGGAGCTCCCTGGAGAGAGGAA	781
Db	1007	AGGCGAGCAACGATATCATGGGTAGTACCAATTTTAAAGGAGCTCCCTGGAGAGAGGAA	1066
QY	782	ACAGAGTGGATGTGCGAGCCAAATATGCTCAACAGAGAGGTTGAGTTTCATTACCCCTC	841

Db 1067 ACAGAGTGGATGCTGCGACGCCAAATAGTCTACCAAGGGAAGGTGAGTTTCATTACCCCTC 1126
QY 842 CTGCAACCTTCAAGAGAGAAAGAAAGAGGAGGAGTGTATGATGAGCTGAAAGTACCAACT 901
Db 1127 CTGCAACCTTCAAGAGAGAAAGAAAGAGGAGGAGTGTATGATGAGCTGAAAGTACCAACT 1186
QY 902 ATAATGAAATCTCTAAATATGGCAAGGAGTACCAAGGAGGAGTGTATGATGAGCTGAAAT 961
Db 1187 ATAATGAAATCTCTAAATATGGCAAGGAGTACCAAGGAGGAGTGTATGATGAGCTGAAAT 1246
QY 962 GGAACCAAGCAACTTAATGAAAGAAAGAAAGGTTTCTAGTAGGCAAGGAGTGTAGGAGG 1021
Db 1247 GGAACCAAGCAACTTAATGAAAGAAAGAAAGGTTTCTAGTAGGCAAGGAGTGTAGGAGG 1306
QY 1022 TGCCCAATCTCTGCTGCTGTGATTAATGAAATGAAATGAAATGAAATGAAATGAAATG 1081
Db 1307 TGCCCAATCTCTGCTGCTGTGATTAATGAAATGAAATGAAATGAAATGAAATGAAATG 1366
QY 1082 GCGCCAGTCATGAGAAATATAATACATGCGAGAAATATCATTTATGTACCCACAGAC 1141
Db 1367 GCGCCAGTCATGAGAAATATAATACATGCGAGAAATATCATTTATGTACCCACAGAC 1426
QY 1142 AAAATAATTTCTACAGGAATAAGGATGCGCAAGGAAAGGCTCTCTGGGGTAGACAAC 1201
Db 1427 AAAATAATTTCTACAGGAATAAGGATGCGCAAGGAAAGGCTCTCTGGGGTAGACAAC 1486
QY 1202 CCCATTCCAAAGGAGGTTTGTCTCCGTAGAGGAGTACAGTAGTGTAGTGTATCTGACA 1261
Db 1487 CCCATTCCAAAGGAGGTTTGTCTCCGTAGAGGAGTACAGTAGTGTAGTGTATCTGACA 1546
QY 1262 GTGGCAGTTCAAGTGAGAGCGATGGTGAC 1290
Db 1547 GTGGCAGTTCAAGTGAGAGCGATGGTGAC 1575

RESULT 7

US-09-794-422-1
; Sequence 1, Application US/09794422
; Publication No. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: P010445
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1655
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-794-422-1

Query Match 31.1%; Score 514.8; DB 12; Length 1655;
Best Local Similarity 63.0%; Pred. No. 1.8e-124;
Matches 994; Conservative 0; Mismatches 487; Indels 97; Gaps 9;

QY 58 TCAATTTTCTAAGTCACTGGGAATAAAGGTTTGGAGTGGAGATGATGCTATCAGC 117
Db 170 TCTGTGAAGCTTGAGCCCTTATGAGGTAAGGAAACAGAGGGTGGCGGAGATGCTCCCTT 229
QY 118 AAACCTACATGACCAAGAAATATGCGCGAGCTCTCATCAGAAATAAATGCAATATA 177
Db 230 CACCTGCTTGACCAGAACAGGAGGTTGCCACCTCTCTCAGAAATATCACTCAGCCTGTA 289
QY 178 ATGGGGCCAGTGACTGCGATTAACCTCTGCGGGGAAGAAACAAAGAGAACACACCTAGG 237

Db 290 AAGAGTCTGTGACGGGGAAGTGAAGTACAGAGCGACAGAAACAAAGAGAAAGAAACCTCAG 349
QY 238 AATGTTCTAAACATATATCCAGCAAGTATGAATTTATGCTAAAGCACACACTCGAAGGATAAA 297
Db 350 AGTGTCTTAAGCGTAAATCCAAAGATGTCACAACTACTAAAGCTACTCAGAAGATACA 409
QY 298 AAGAGCCTCAAGAGATTTCCCAAGCCCAAGAAAGTCCAGTAAAGAGCAAAAGCACCCTAT 357
Db 410 GAGAACCAACAGAGGGATCTACTACTCCAGAACAGCCCAAGCAAGCAAAAGCAACACCCCT 469
QY 358 CGTATTCAACACAAATGACTACTTAAACATCTCTCAAAAGTCAAAAGTCAAAAGTCAAAAGT 417
Db 470 CGGGCCGAGAGACAGCAGCTACCTTAACACATCTCCCCAATCAGAAGATTTCTCAGT 529
QY 418 GATTTTGAAGGAGCGGTTTATACAGATCTTCAAGAGAGAGGGGACAAATGATATATCTCCT 477
Db 530 GACTTCGAGGACAGTGTCTCCAGACCTTCTAGTGAGGGGGATTAATGATGTCCCTCCT 589
QY 478 TTCAAGTGGGAGCGCCCACTTTTAAAGACATTTCTGGTAAAGGAGAGTACTGTGCTCT 537
Db 590 TTCAAGTGGGAGTGGACCAATTTTATGACACTCCCGACAGAGAGGAGTGTCTGTGGATCT 649
QY 538 GACCTAGAGGCAAGATATTCAAACAGGTTTGCAGGCCCAAGTGAAGCTGAGAGTACT 597
Db 650 GATCTGAAAGCTCAGCTGCTGCTCCTCTGTGT --- CAGGCTCCAGCAATGTCTGAGATTGTT 706
QY 598 CATCTTGCACAAAAAGCCAGGTTTATATGAGATCCCAAGAGAGAGAGAAAGTGTGGGA 657
Db 707 GACCCACACACGATGAGTGTGGCTCTAATGAGATCCAGGAGAGAGAGTGTGATAGGC 766
QY 658 AATACATTTGAACTAGGATGAACTGCGAAAGAGGAGAGTGTCTTGTGATGTGAGCTT 717
Db 767 GGTGCTTATGCAACAGAGAGAAAGTGTGCGAGGGGGCAGGTTCCCGGAGTGTGAGCTT 826
QY 718 GTAGAGGGCAGCAACGATATCATGTGTAGTACCAATTTTAAAGAGGCTCCCTGGAAGAA 777
Db 827 GTGAGAGGGCAGCAATGAAATCAGGGGAGTACCAATTTAGGGAGTCTCCCTGGAAGAA 886
QY 778 GGAACAGAGTGGATGCTGGCAGCCAAATGCTCAAGGGAAGGTTGAGTTTCAATTAC 837
Db 887 GGAACAGAGTGGATGCTGGCAGCCAAATGCTCAAGGGAAGGTTGAGTTTCAATTAC 946
QY 838 CTTCTGCAACCTTCAAGAGAGAAAGAAAGAGGAGTGTGATGATGATGATGATGATGATGAT 897
Db 947 CCACAAAGGCGCTCAAAAGAGAGAGTAAAGGGGCGAGCAGGAGGACACACAGGGAAGCC 1006
QY 898 AACTATAATGAAATTTCTTAAATGCGAAAGCAGTACCAAGAGAGGTTGATGATGATGATGAT 957
Db 1007 GGTTCATGAAATCCCAAGAGCAGAGGCGGCGCTAGCAAGGATCGGGAAGATCT 1066
QY 958 AATAGGAACCAAGCAACCTTAAATGAAAGAAAGGTTTCTTAGTAAGGGCAAAAGTCTAG 1017
Db 1067 AAAGGGAACCAAGTAACTTGTACTGAAGCCAAAGTTCCAGGCAAGAGCAAGGCGCAG 1126
QY 1018 GGCCTGCGCCATCTCTTCTGCTGCTTGTATGATGAAATCAAAAGTCAAAAGTCAAAAGT 1077
Db 1127 -----TCTTCTCAGAGTCTTGTGATGAGGTTAAAGTGAAGAGACTCTTCT 1174
QY 1078 AATGCGCCAGTCAATGAGAAATATATACATGCGCAAGAAATATCATTTATGTACCCAC 1137
Db 1175 AATAGTCTCAGTAGAGAGGAGTGTGCAATA -----GCACACAGG 1213
QY 1138 AGACAAAATAATTTCTACACGGAATAAGGTTATGCGACAGGGAAGGCTCTCTGGG ---GT 1194
Db 1214 AGAACAGCCACCTTACACGGAATAGGGGATGTACAGCGGAGAGGCTCTCTGGGCTCG 1273
QY 1195 AGACAAACCCATTTCAACAGAGAGGTTTGTGTTCCCGTAGAGGATGACAGTAGTAGTCA 1254
Db 1274 AGAAGACCCATTCGCCACCGCGGGTGAAGCACCCGCCAAAG ---AGACAGTAGTAGTCA 1330
QY 1255 TCTGACAGTGGCAGTTCAAGTGAGAGGATGGTGTAGTGTATGATGATGATGATGATGATGAT 1314

Db 1331 TCATCCAGTGGAGTCTTAGCGAGAGCAGTGGTGAAGTCTAGACCCCGGGTTGAACAGTT- 1389
Qy 1315 GGTGACAGTCTGAAGACCTCGTCACTGTGAGTGTAGAGGAGAGCACCCTGACAGC 1374
Db 1390 -----CCAGCTCT 1398
Qy 1375 TGACCAAGTGAAGAGAGATAGAGTGAAGAACTGAGTGAGCAGCAAGAAATCTCTGGTCTCTT 1434
Db 1399 GGTCTGGAGAAAGAGAGGAGCGCAGCAGGAGCTGAGCAAGGTACACAGTGTGTCACCTC 1458
Qy 1435 GGGGGAATTTTGTCTATTAATAGTACAGATATAAAATTTCTATTAAGAGGTATAATGTT 1494
Db 1459 CA-GGACACTGTGCTGTGTGTGTGTTGTTGTAATAAGAAATCCTACTCAAAGTTCTAATGCT 1517
Qy 1495 TTTAAGCAAAAAAATCATTACAGATCTATGAATAGGTAAACNTTTGAGTAGTGTGTCAT 1554
Db 1518 TTCTGAATAAAACCTTTGGAAG-ATTATATAATAGGTAAATTTGACTAGCGGCC 1576
Qy 1555 TTAATAATAGTGTGTAATGTCAAAATGCTTC-TATGTTGTTTGTCTCTGTAGACATGA 1613
Db 1577 ATTAATAATAGTGTGAGTGTACAGGTGCTTGATATGATATGATTTGCTTTCAGACATGA 1636
Qy 1614 AATAAACAATATCTCTC 1631
Db 1637 AATAAAGAGGCTTTCTC 1654

RESULT 8

US-09-794-422-3
; Sequence 3, Application US/09794422
; Publication No. US2003016629A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patent-In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1682
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-794-422-3

Query Match 29.3%; Score 485.2; DB 12; Length 1682;
Best Local Similarity 62.3%; Pred. No. 1.1e-116;
Matches 1017; Conservative 0; Mismatches 483; Indels 132; Gaps 11;

Qy 16 AGTATCAGTAAACAAGAGATACTCAATGGCTGAGGATGTCATTTATCTTAAGTCA 75
Db 166 AGCTGGGCAATCAAGACGATTCACAGGACTTGGCAGCATCTGTGTATCTGATCCC 225
Qy 76 ACTGGGAATTAAGGGTTTGAGGATGAGATGCTATCAGCAAACTACATGACCAAGAA 135
Db 226 ACGGTGGATGAAGGCACAGAGGATGGCAAGGTGCTCTCTTCCACCGCTGGCCAGGAC 285
Qy 136 GAATATGGCGCAGCTCTCATCAAAATACATCAACATATATATGGGCCAGTGTGCG 195
Db 286 AGTATGTTGCTGCTCCCTCTCTCAGAAATATACCCAGCCTGTAAAGAGTCTAGTGA 345
Qy 196 ATTAATACTCTGGGGGAAGAAACAAGAGAAACACACCTAGGAATGTTCTTAACAATA 255
Db 346 GCGGAATACGGAGGAAGAAACACAGGAGAGACCTCAGAGTGTCTTACCGTAAT 405
Qy 256 CAGCAAGTATGTAATTATGCTAAGACACTCGAAGGATAAAGAGGCTCAAAGAGAT 315
Db 406 CCAGCAGATGTAATGATGCTAAAGTCTCTTAAAGACATAAAGAAATCAAGAGTTAT 465
Qy 316 TCCCAAGCCAGAAAAGTCCAGTAAAG-----CAAAAGCACCCTCGTATTCAA 366
Db 466 CTGCTAACCCAGAGCAGCCGGTCAAAAGCAAAACACACACACCCGACACCGA 525
Qy 367 CACACATTTGACCTACCTAAACATCTCTCAAAAGTCAAAATAATCCCAAGTATTTGAA 426
Db 526 CGGAGCACTCACTACCTGACACATCTCCACAGATCAAGAGACTCCCAAGTATTTGAA 585
Qy 427 GGCAAGGTTATACAGATCTTCAAGAGAGAGGGGACATATATATCTCTTCAAGTGG 486
Db 586 GGCAAGTGGTCTCCAGATCTTCTAGTGGGGAGATAATGATGTCCTCCCTTTTCAAGTGA 645
Qy 487 GACGGCCAACTTTTAAAGACATTTCTGTGTAAAGGAGAGCTACTGTCTCTGACTAGAA 546
Db 646 GATGGGCAACATTTTATGCACATTTCTGTGCAAAAG---AGTGTCTGGTCTGTCTTGA 702
Qy 547 GGCAAGATATTCACACAGGGTTTGCAGGCCCAAGTGAAGTGAAGTGAAGTACTCATTTGAC 606
Db 703 AGCTCAACTAGTCTGCCC---CCTCTCAGGCTCCAGCAAGCTGAAGTTATTTGACCCAT 759
Qy 607 AAAAAAGCCAGCTTATATAGATCCACAGAGAGAGAAATATGCTGGAATACCAT 666
Db 760 ATGAGTGGACTAGCTCTAATGAGATCCCGGGAGAGAGACATGTTGGCAGTGCCTAT 819
Qy 667 GGAATAGGGATGAATCTGCAAGAGAGGAGAGTCTGTTGATGTGCTGAGCTTTGTAGAGGC 726
Db 820 GCAACAGAGACAAAGCTGCACAGGGGGCAGGCTCTGCAGTGGAGCCTTTGTGGGGGC 879
Qy 727 AGCAACGATATCATGGTAGTACCAATTTTAAAGAGTCTCTCGAAGAGAGAGAAACAGA 786
Db 880 AGCAATGAATTCACAGCAGCAACCAATTTTCAAGGAACTCCCGAAAGAGAGAAACAGA 939
Qy 787 GTGGATGCTGGCAGCCAAATGCTCACAGAGGAAGTTCAGTTCATTTCAATCCCTCTGCA 846
Db 940 ATTAATGCGGAGCAGCAAAATGCTCATCAAGGAAAGTAAATTTTCAATTCACAAAGTG 999
Qy 847 CCTCAAAAGAGAAAAAGAAAGGAGGAGTGTGATGATGAGTCAAGTGAAGTCAACATAAT 906
Db 1000 GCCTCGAGAGAAAGGTAAAGGGGGCGTGGAGCATGCA---GGAGAGCTGGTTACAAC 1056
Qy 907 GAAATTCCTAAATGCGAAAGCAGTACCAAGAAAGGTGTAGTCAATTTCTATAGAAC 966
Db 1057 GAAATCCCAAGAGCAGCAAGGTAGCTCTAGCAAAAGATGCAGAAAGTCCAAAGGAAAC 1116
Qy 967 CAAGCAACTTAAATGAAAAACAAAGGTTTCTAGTAAAGGCAAAAGTCAAGGCTGCCCC 1026
Db 1117 CAATTAACCTTGTCTGCAAGCCAAAGATTTCCAGGTAAGGCAAAAGCCAGGCGCTGCT 1176
Qy 1027 ATTCCTTCTGTTGCTTGTGATAATGAATCAAAAGCAAAATGATGATTCCTTTAATGGCCC 1086
Db 1177 CTGCCCTCTCACAGTCTTAGTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1214
Qy 1087 AGTCATGAGATATAATAACACATGCGCAAAATATCATTTATGTAACCAACAGACAAAAT 1146
Db 1215 -----AGAAACCAATATGTTTCCATGACAAAAT 1245
Qy 1147 AATTCTACAGGAATAAGGATAGCCACAGGAGAAAGGCTCTCTGGGT---AGACAACCC 1203
Db 1246 AATCTTACCCGATTAAGAGATGTCACAGCGAGAGGCTCTCTGGCTTCGAGAAAGACC 1305
Qy 1204 CATTCACAGAGGTTTATGTTCCCGTAGAAGGATGACAGTAGTGAAGTCAATCTGACAGT 1263
Db 1306 AATTCCACAGCGCGCTAGACCCGCCAAAG---AGACAGCAGCAGTCTGTCATCAGT 1362
Qy 1264 GGCAGTTCAAGTGAAGAGCATGCTGATAGTCCACAGAGGTTCCAGCGGGGTGACAGT 1323
Db 1363 GGGAGTTCTAGTGAGAGTCAATGCTAGTCTCTGGGATGAAACCAAGT----- 1411
Qy 1324 CTGAAGACCTCGTCTGAGTTGATGTAGAGGAGAGCCACCTGACAGTGAACAGGT 1383


```
Db 1412 -----CCCTGCTCTAGTCTCGAG 1431
QY 1384 GAAGACAGATAGACTGAGAACTGAGTGAGCCAGATCTGCTCTCTGGGGGAATT 1443
Db 1432 GAAGAGAGGCGACAG-CAGGAAGTGAAGCCAGCCAGACCTGGTCCCTCCAGGACA-T 1489
QY 1444 TTGTCTATCTTAATAGTACAGATATAAAATTTCTATTAAGGCTATTAATGTTTTTAAGCAA 1503
Db 1490 TGTGCTATTTTAAATGTTGTTTAAAGATTTCTACTCAAGTTCTTAATGCTTTTTCAT 1549
QY 1504 AAAAAATCATTTACAGATCTATGAATAGGTAAACATTTGATGAGTGTCTATTTTAAAAATA 1563
Db 1550 AAAAACTTTTATAAAGATTTGTATAATAGGTAATTTTGACAGGCGACACATTTAAAAATA 1609
QY 1564 GTTGTGTAATGTCACAAATGCCCTT-----CTATGTTGTTGCTCTGTAGACATGAATAAA 1619
Db 1610 GTCTGTAATGTCACAAATGCCCTTGATGATCATCTTTGCTCTTTCAGACATGAATAAA 1669
QY 1620 ACAATATCTCTC 1631
Db 1670 ATATGCTTGCTC 1681

RESULT 9
US-09-908-975-16013
; Sequence 16013, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16013
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-16013

Query Match 3.6%; Score 60; DB 12; Length 60;
Best Local Similarity 100.0%; Pred. No. 7.8e-06;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1369 GACAGCTGACAGGTGAAGAGAGGATAGAGTGAAGAACTGAGTGAGCCAGAAATCTCTGCT 1428
Db 1 GACAGCTGACAGGTGAAGAGAGGATAGAGTGAAGAACTGAGTGAGCCAGAAATCTCTGCT 60

RESULT 10
US-10-312-841-1/c
; Sequence 1, Application US/10312841
; Publication No. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
; FILE REFERENCE: E01/1208/WO
; CURRENT APPLICATION NUMBER: US/10/312,841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 3673778
; TYPE: DNA
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3294164)
US-10-312-841-1

Query Match 2.9%; Score 47.6; DB 12; Length 3673778;
Best Local Similarity 51.9%; Pred. No. 13;
Matches 107; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 1450 ATCTTAATAGTACAGATATAAAATTTCTATTAAGGCTATTAATGTTTTTAAGCAAAAAA 1509
Db 2056906 ACTTAACACTTATATATCAAAACACTTCTTAAATTTTACAAATCAACTCATTTAATC 2056847
QY 1510 ATCATTTACAGATCTATCAAAATAGGTAAACATTTGAGTAGGTGTCATTTAAAAATAGTTGGT 1569
Db 2056846 CTCCTAAATACCTCTAAATATAATATACTATTTCGATCTCTTTCTTATAAAAAACCCAT 2056787
QY 1570 GAATGTCACAAATGCCCTTCTATGTTGCTCTGTAGACATGAAATATAACAATATCTC 1629
Db 2056786 TTTTTTTTCTCTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 2056727
QY 1630 TCGATGATAAAAAAATAAAAAA 1655
Db 2056726 TCTATCACCCTAAATTAATAACAATA 2056701

RESULT 11
US-09-814-353-5466/c
; Sequence 5466, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5466
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 115, 144, 153, 155, 156, 157, 161, 163, 164, 167, 168, 170,
; LOCATION: 171, 172, 173, 179, 186, 187, 189, 190, 192, 194, 195, 196,
; LOCATION: 197, 200, 201, 202, 206, 207, 209, 211, 231, 256, 257, 265,
; LOCATION: 272, 273, 274, 276, 283, 287, 288, 290, 291, 293, 295
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 309, 314, 315, 327, 331, 332, 333
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-5466
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Query Match 2.8%; Score 46.8; DB 12; Length 345;
Best Local Similarity 46.8%; Pred. No. 0.068; 92; Indels 0; Gaps 0;
Matches 81; Conservative 0; Mismatches 92; Indels 0; Gaps 0;
QY 1483 GGCTATAATGTTTTTAAGCAAAAAAATCATTACAGATCTATGAAATAGGTAACTTG 1542
DB 260 GGGNNNTTTTTTTTAAATAAAAAAATTTTTTTTTTTTTTTTTTTNNNNGGNN 201
QY 1543 AGTAGGTGTCATTAAATAAGTTGGTAATGTCACAAATGCCCTTCTATGTTGTCCTC 1602
DB 200 NTNNNGNGNNTNNNAANAATTTTTNNNNNTNNAANGNTTTNNNTNTTTTTTTNAGG 141
QY 1603 TGTAGACATCAAAATAACCAATCTCTCGATGATATAAAAAAATAAAAAA 1655
DB 140 GGGGGAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 88

RESULT 12

US-09-814-353-11753/c
; Sequence 11753, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11753
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 115_144, 153, 155, 156, 157, 161, 163, 164, 167, 168, 170,
; LOCATION: 171, 172, 173, 179, 186, 187, 189, 190, 192, 194, 195, 196,
; LOCATION: 197, 200, 201, 202, 206, 207, 209, 211, 221, 256, 257, 265,
; LOCATION: 272, 273, 274, 276, 283, 287, 288, 290, 291, 293, 295
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 309_314, 315, 327, 331, 332, 333
; OTHER INFORMATION: n = A,T,C or G

US-09-814-353-11753

Query Match 2.8%; Score 46.8; DB 12; Length 345;
Best Local Similarity 46.8%; Pred. No. 0.068; 92; Indels 0; Gaps 0;
Matches 81; Conservative 0; Mismatches 92; Indels 0; Gaps 0;
QY 1483 GGCTATAATGTTTTTAAGCAAAAAAATCATTACAGATCTATGAAATAGGTAACTTG 1542
DB 260 GGGNNNTTTTTTTTAAATAAAAAAATTTTTTTTTTTTTTTTTTTNNNNGGNN 201
QY 1543 AGTAGGTGTCATTAAATAAGTTGGTAATGTCACAAATGCCCTTCTATGTTGTCCTC 1602

DB 200 NTNNNGNGNNTNNNAANAATTTTTNNNNNTNNAANGNTTTNNNTNTTTTTTTNAGG 141
QY 1603 TGTAGACATCAAAATAACCAATCTCTCGATGATATAAAAAAATAAAAAA 1655
DB 140 GGGGGAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 88

RESULT 13

US-10-032-585-6930
; Sequence 6930, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6930
; LENGTH: 2826
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-6930

Query Match 2.8%; Score 46.6; DB 12; Length 2826;
Best Local Similarity 51.2%; Pred. No. 0.28;
Matches 109; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
QY 951 TCATTCTAATAGGAACCAACCTTAATAATGAAAAACAAGGTTCTCTAGTAAGGCAA 1010
DB 21 TCCTAATAATAATAATAAATTCAGACATCAATCTCCACAGGGCTCTCTCCAATAAGT 80
QY 1011 AAGTCAGGGCCTGCCATTCTCTCGTGTCTTGTATGAATCAAAACGAAATGGA 1070
DB 81 AATATTGGCGATTCAATTTTGGTCTTGGTATATGTAGTTATTATTAATGATAACA 140
QY 1071 TTCCTTTAATGGCCCGATCATGAGAAATATAACACATGGCAGAAAAATATCATATGT 1130
DB 141 AACTCATATTAAACATACACCTTATTAATATCACCATAATCTTGATAAAATCTCATGT 200
QY 1131 ACCCCACAGCAAAAATAATTTCTACCGGAATAA 1163
DB 201 AACCACTTTACAAAAATAATTTTACCACCAATAA 233

RESULT 14

US-09-887-576-831/c
; Sequence 831, Application US/09887576
; Patent No. US20020144047A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, P.
; APPLICANT: Brown, D.
; APPLICANT: Chang, H.
; APPLICANT: Zhu, T.
; APPLICANT: Han, B.
; APPLICANT: Wang, X.
; APPLICANT: Cooper, Bret
; TITLE OF INVENTION: Promoters for regulation of plant expression
; FILE REFERENCE: 1360.001US1
; CURRENT APPLICATION NUMBER: US/09/887,576
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,848
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/214,087
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/258,692
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 875
; SOFTWARE: FastSeq for Windows Version 4.0


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; SEQ ID NO 831
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-887-576-831

Query Match      2.8%; Score 45.8; DB 10; Length 2000;
Best Local Similarity 53.0%; Pred. No. 0.37;
Matches 98; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 1471 AATTCTATTAAAGCGTATAATGTTTTTAAGCAAAAAAATCATTCAGATCTATGAAAT 1530
Db      |||||
QY 1531 AGGTACATTTGAGTAGGTCATTTAAATAAGTTGGTGAATGTCACAAATGCCTTCTA 1590
Db      |||||
QY 1209 AAGTAGTTTAGGCAATGCTTAAATCAATCTTAGGAATATAATCATAAATAACITTTA 1150
Db      |||||
QY 1591 TGTGTTTGGCTCTGTAGACATGAAATAAACAATATCTCTCGATGATAAAAAA 1650
Db      |||||
QY 1149 AGTTGTGAGTTGAAATATAAATAATATATATATAGATTGTCCTTGAAAAATAATTT 1090
Db      |||||
QY 1651 AAAAA 1655
Db      |||
QY 1089 TATAA 1085
Db      |||

RESULT 15
US-10-312-841-2/c
; Sequence 2, Application US/10312841
; Publication No. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
; FILE REFERENCE: E01/1208/WO
; CURRENT APPLICATION NUMBER: US/10/312,841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (379615)
US-10-312-841-2

Query Match      2.7%; Score 44.8; DB 12; Length 3673778;
Best Local Similarity 50.5%; Pred. No. 70;
Matches 109; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 1440 AATTTTGGCTATCTTAATAGTCACAGTATAAAATTCATTAAAGGCTATAATGTTTTAA 1499
Db 1030117 ATCTTTTCAAAATTATAACAAATATACCACACTAATATAAATATTATAATAACAAA 1030058
QY 1500 GCAAAAAAATCATTCACAGATCTATGAATAGTAGTAACATTTGAGTAGGTCATTTAA 1559
Db 1030057 ATAAAAA 1029998
QY 1560 AATAGTTGGTGAATGTCACAAATGCCTTCTATGTTGCTCTGTAGACATGAAATAA 1619
Db 1029997 AATCTAAACTATCTTTAAATAATAATCTATTAAATTTTTTTTTTAAAAA 1029938
QY 1620 ACAATATCTCTCGATGATAAAAAA 1655
Db 1029937 ACTAATACACTATATAACATAAAAAAACTCTAAAAA 1029902

Search completed: November 29, 2003, 22:35:57
Job time : 543 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 26, 2003, 15:45:42 ; Search time 21 Seconds
(without alignments)
866.365 Million cell updates/sec

Title: US-09-700-696C-2

Perfect score: 2279

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	140	6.1	772	1	US-08-524-757-12
2	136	6.0	1187	1	US-08-320-559-28
3	136	6.0	1187	3	US-08-545-860D-28
4	136	6.0	1187	5	PCT-US94-04496-28
5	136	6.0	1210	1	US-08-320-559-26
6	136	6.0	1210	3	US-08-545-860D-26
7	136	6.0	1210	5	PCT-US94-04496-26
8	135.5	5.9	723	1	US-07-814-964-11
9	135.5	5.9	723	1	US-08-258-442-11
10	135.5	5.9	723	1	US-08-328-809-6
11	135.5	5.9	723	4	US-08-866-840-6
12	135.5	5.9	723	5	PCT-US92-11107-11
13	134.5	5.9	1115	2	US-08-568-459A-2
14	134.5	5.9	1115	2	US-08-487-826B-2
15	134.5	5.9	1115	4	US-09-210-288-2
16	134.5	5.9	1115	6	5198347-6
17	128	5.6	703	3	US-08-910-925-4
18	127.5	5.6	1235	1	US-08-118-101A-2
19	126.5	5.6	455	5	PCT-US93-07261-13
20	126.5	5.6	1663	3	PCT-US93-07261-16
21	125.5	5.5	1261	3	US-09-208-742-4
22	125.5	5.5	1261	4	US-09-332-295-2
23	125.5	5.5	1261	4	US-09-709-979-2
24	124.5	5.5	1183	4	US-09-134-001C-3530
25	123	5.4	493	3	US-08-999-774A-12
26	123	5.4	1177	4	US-09-134-001C-5106
27	123	5.4	1588	5	PCT-US93-07261-11

Sequence 12, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 37,345
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Patent No. 5198347
Sequence 4, Appl
Sequence 2, Appl
Sequence 13, Appl
Sequence 16, Appl
Sequence 4, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 3530, Ap
Sequence 12, Appl
Sequence 5106, Ap
Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-524-757-12
; Sequence 12, Application US/08524757
; Patent No. 5792634
; GENERAL INFORMATION:
; APPLICANT: Conaway, Ronald C.
; APPLICANT: Conaway, Joan W.
; APPLICANT: Bradsher, John N.
; TITLE OF INVENTION: RNA Polymerase Transcription Factor
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS
; STREET: 1201 Elm Street, Suite 4500
; CITY: Dallas
; STATE: TX
; COUNTRY: US
; ZIP: 75270-2197
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/524,757
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13621
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160087
; FILING DATE: 30-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Harre, John A.
; REGISTRATION NUMBER: 37,345
; REFERENCE/DOCKET NUMBER: B35006CIPCIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (214) 939-4500
; TELEFAX: (214) 939-4600
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 772 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-524-757-12

Query Match 6.1%; Score 140; DB 1; Length 772;
Best Local Similarity 20.5%; Pred. No. 0.0014;
Matches 87; Conservative 49; Mismatches 144; Indels 144; Gaps 17;

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QY 23 PKSTGNKGFEDGDAISKLHDOEYGAALINNNQHIMGPVTAIKLGEENKENTPRNVL 82
D 210 PKGHSNAFQRLGASQERHLGEPHGKGVQSNKEH----- 245
QY 83 NIIPASMYAKAHKDKKKPORDSOAKSPVKSKSTHRIQHNDYLVKLSKVKIPSPDFE 142
D 246 -----KSSHKKRPVDAKDEKASVVSREKSH-----KALSK----- 277
QY 143 GSGYTDLOERGDNDISPFSGDQGPQKDIIPGKGATGPDLEKGIQTGFAGPSEAES-THL 201
D 278 -----EENRRPSPGDNAREKP-PSSGVKKEKDREGSSLLKKCLPPSEASDNHL 325
QY 202 DTKPGYNEIPEREENGNTTGTDRDETAKEADADVSLVEGSDNIM-----GSTNFKEL 255
D 326 -----KKPKHRD-PEKAK-----LDKSKQGLDSFDTG--KGAGDLLPKVKEKGSNNLKTP 372
QY 256 PGREGRNVDAGSONAQHOKV-----EFHVP-----PAPSKERKEGSSDAES 298
D 373 EGKVTNLDKSLGS-LPKVETDMEDEFEQTMSFESYLSYDQPRKKKKIVKT-SATA 430
QY 299 TNYNEIPKNGKSTRKGVHDHNRNQATLNEKQRPSPKSGSQGL----- 341
D 431 LGDKGLKNDKSKSTGKNLDSVQKLPKVNKTSEKEPAGADLAKLRKVPDVLPLPLPA 490
QY 342 -----PIPSGLDNEIKNEMDSFNGPSHEN-----IITHGRKYHVHP----- 378
D 491 IQANYRPLPSLELSSFPKPKAFSSPQEBEAGFTGRMNSKMGVYSGSKCAYLPKMMT 550
QY 379 -HQ 381
D 551 LHQQ 554

RESULT 2
US-08-320-559-28
; Sequence 28, Application US/08320559
; Patent No. 5633135
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Canaani, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods for
; TITLE OF INVENTION: Detection and Treatment of Acute Leukemias
; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the
; TITLE OF INVENTION: All-1 Region
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5633135ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,559
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/062,443
; FILING DATE: 14 MAY 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/971,094
; FILING DATE: 30-OCT-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/888,830
; FILING DATE: 27-MAY-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/805,093
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; FILING DATE: 11-DEC-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-0855
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-320-559-28

Query Match 6.0%; Score 136; DB 1; Length 1187;
Best Local Similarity 20.6%; Pred. No. 0.0058;
Matches 86; Conservative 52; Mismatches 166; Indels 114; Gaps 14;

QY 92 AKAHSKDKKKPORDS-----QAQSPVKSKSTHRIQHNDYLVKLSKVK 135
D 530 SOEHSESKDPPPKSSSKAPRAPPEAPHPGKESCKSPQAQPPQQTGTGKPK-----K 584
QY 136 KIPDFEGSGVTDLOERGDNDISPFSGDQGPQKDIIP-----GKGE-----ATGPD 181
D 585 PVKASARAGSRTSLQGEREPGLLPYGRSDQTSKDKPVKTKGRPRAAASNEPKPAVPPSS 644
QY 182 EGKDIQTGFAGPSEAES-----THLDTKPGY-----NEIPEREENGNTTGTDR 227
D 645 EKKHKSLPAPSKALSGPEPAKONVEDRTEHFALVPLTSEQPPHSGSRTSGCQA 704
QY 228 TAKEADADVSLVEGSDNDIMGSTNFKELPGREGNRV-----DAGSONAQHOKVE 276
D 705 VVQEDSKRDLPLPLRDTKLLSPRLDTPPQSLMWKITLLSLRIPOPPGKSGRQKAE 764
QY 277 FHYPPAPSKERKKGSSDAEAESTYNEIPKNGKSTRKGVHDHNRNQATLNEKQRPSPKG 336
D 765 DKQPPAGKHSSEKRSDDSS-----SKLAKRKGEARDCD-----NKKIR----- 805
QY 337 KSQGLPIPSRGLDNEIKNEMDSFNGPSHENIIT-----HGRKYHVHPHQRNNSTRNK 388
D 806 -----LEKEIKSQSSSSSSSHKESKTKPRSPSSQSSKEMLPPIPPVSSSQKP 854
QY 389 GMPQKGSG-----WGRQP-----HSNRRFSRRRRDSSSDSGSSSE-----SDGD 430
D 855 AKPALKSRREADTCGQDPPKASSTKSNHKDSITPKQRRVEGKRSRSSSEHKGSSGD 912

RESULT 3
US-08-545-860D-28
; Sequence 28, Application US/08545860D
; Patent No. 6040140
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Canaani, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
; TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1 Region
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
; ADDRESS: NO. 6040140ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,860D
FILING DATE: 07-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04496
FILING DATE: 22-APR-1994
PRIOR APPLICATION DATA: PCT/US92/10930
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/327,392
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/320,559
FILING DATE: 11-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,443
FILING DATE: 14-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/971,094
FILING DATE: 30-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,839
FILING DATE: 27-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/805,093
FILING DATE: 11-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Deluca Esq., Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1262
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-545-860D-28

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[illegible]

DB 855 AKPALKSRREADTCGDDPKPSASTSNHKKDSSIPKORRVEGKGRSSSEHKSSGD 912

RESULT 4
PCT-US94-04496-28
; Sequence 28, Application PC/TUS9404496
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Canaani, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
; TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
; ADDRESSEE: Norris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04496
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca Esq., Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1242
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-04496-28

Query Match	6.0%;	Score 136;	DB 5;	Length 1187;
Best Local Similarity	20.6%;	Pred. No. 0.0058;		
Matches	86;	Conservative	52;	Mismatches 166;
			Indels 114;	Gaps 14;
QY	92	AKAHSKDKKPKQDS-----	QAQKSPVKSSTHRIQHNIDYLKLSVKV	135
Db	530	SQSHSGDKPPKSSSKAPPAPEAPHGPKRSCQKSAQOEPPQRTVGTKPQK-----	K 584	
QY	136	KIPDFEGSGYTDLQERGDNDISFSGDGQPFKDIP-----	KGKE-----	ATGPD 181
Db	585	PVKASARAGSRTSLQEREPGLLPYGSRDQTSKDKPKVTKGPRAASNEPXPAPVPSS	644	
QY	182	EGKDIQTGFAGPEARS-----	THLDTKPGY-----	NRIPERENGNNTIGTRDE 227
Db	645	EKKHKHSLPAPSKALSGPEPAKNDVEDRTPHFALVPLTESQCPHSGSGSRSTGCRQA	704	
QY	228	TAKEADAVDVSLVEGSDIMGSTNFKELPREGNRV-----	DAGSQNAHQKVE	276
Db	705	VVVQEDSRKDRLEPLPDRDTKLLSLPDRTPPPQSLMKWLTLLLSRLPQPPKSGSRQKAE	764	
QY	277	FHYVPPAPSKERKKEGSDDAABESTNYNEIPKNGKSGTRKGYDHSNRNQATLNEIKQRFPSKG	336	
Db	765	DKQPPAGKSHSSEKSSDSS-----	SKLAKRKGEAERDC-----	NKKIR----- 805
QY	337	KSQGLPIPSRGLDNEIKNEMDSFNGSHENIIT-----	HGRKYHYVPHRONNSTRNK	388
Db	806	-----	LEKEIKSOSSSSSHKSSSKTKPRPSQSSKXEMLPPLPPPVSSSSQKP	854


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; NAME: Deluca Esq., Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1262
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1210 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-04496-26

Query Match      6.0%; Score 136; DB 3; Length 1210;
Best Local Similarity 20.6%; Pred. No. 0.0059;
Matches 86; Conservative 52; Mismatches 166; Indels 114; Gaps 14;

QY 92 AKAHSDKKKKPQDSDS-----QAQKSPVKSKSTHRIQHNIDYILKHLKSVK 135
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
553 SQEHSSEKDPKPKSSSKAPRAPEAPHPGKRSCKSPAQOEPPQRTVGTGKQPK-----K 607
QY 136 KIPSPFEGGYTDLQERGNDISPPSGDQPPKDIP---GKGE-----ATGPD 181
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
608 PVKASARAGSRTSLQGEREPGLPYGSRDQTSKDKPKVTKGRPRAAASNEPKPAVPPSS 667
QY 182 EGKDIQTGPAGPSEAES-----THLDTKKPGV-----NEIPEREENGNTIGTRDE 227
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
668 EKKGKSSLPAPSKALSGPEPAKDNVEDTPEHFALVPLITESQGPSPHSGGRTSGCROA 727
QY 228 TAKEADADVSVLVEGNDIMGSTNFKEPFGREGNRV-----DAGSQNAHQKVE 276
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
728 VVQEDSRKDRPLPLRDTKLLSPLRDTPPQSLMVKITLDLLSRIPQPPGKSGRQKAE 787
QY 277 FHPVPAPSKKEKEGSSDAESTNNEIPKNGKSTRKGVDSNHNQATLNKQRPSPKG 336
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
788 DKQPPAGKHSSEKSSSDSS-----SKLAKRKGAEARDCD-----NKKIR----- 828
QY 337 KSQGLPIPSRLGDLNBIKNEMDSFNGPSPHENIIT-----HGRKVYVYVPHQNNSTRNK 388
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
829 -----LEKIKSQSSSSSSSHKESKTKSPRSPSSQSKKEMLPVPPVSSSSQKP 877
QY 389 GMPQKGS-----WGROP-----HSNRRFSSRRRDDSSSDSGSSSE---SDGD 430
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
878 AKPALKRSRRADTCQDPPKPSASSTKSNHKDSSIPKQRRVEGKSGRSSEHKSGSD 935

RESULT 7
PCT-US94-04496-26
; Sequence 26, Application PC/TUS9404496
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Cnaan, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
; TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
; ADDRESSEE: Norris
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04496
; FILING DATE:
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; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca Esq., Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1242
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1210 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-04496-26

Query Match      6.0%; Score 136; DB 5; Length 1210;
Best Local Similarity 20.6%; Pred. No. 0.0059;
Matches 86; Conservative 52; Mismatches 166; Indels 114; Gaps 14;

QY 92 AKAHSDKKKKPQDSDS-----QAQKSPVKSKSTHRIQHNIDYILKHLKSVK 135
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
553 SQEHSSEKDPKPKSSSKAPRAPEAPHPGKRSCKSPAQOEPPQRTVGTGKQPK-----K 607
QY 136 KIPSPFEGGYTDLQERGNDISPPSGDQPPKDIP---GKGE-----ATGPD 181
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
608 PVKASARAGSRTSLQGEREPGLPYGSRDQTSKDKPKVTKGRPRAAASNEPKPAVPPSS 667
QY 182 EGKDIQTGPAGPSEAES-----THLDTKKPGV-----NEIPEREENGNTIGTRDE 227
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
668 EKKGKSSLPAPSKALSGPEPAKDNVEDTPEHFALVPLITESQGPSPHSGGRTSGCROA 727
QY 228 TAKEADADVSVLVEGNDIMGSTNFKEPFGREGNRV-----DAGSQNAHQKVE 276
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
728 VVQEDSRKDRPLPLRDTKLLSPLRDTPPQSLMVKITLDLLSRIPQPPGKSGRQKAE 787
QY 277 FHPVPAPSKKEKEGSSDAESTNNEIPKNGKSTRKGVDSNHNQATLNKQRPSPKG 336
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
788 DKQPPAGKHSSEKSSSDSS-----SKLAKRKGAEARDCD-----NKKIR----- 828
QY 337 KSQGLPIPSRLGDLNBIKNEMDSFNGPSPHENIIT-----HGRKVYVYVPHQNNSTRNK 388
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
829 -----LEKIKSQSSSSSSSHKESKTKSPRSPSSQSKKEMLPVPPVSSSSQKP 877
QY 389 GMPQKGS-----WGROP-----HSNRRFSSRRRDDSSSDSGSSSE---SDGD 430
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
878 AKPALKRSRRADTCQDPPKPSASSTKSNHKDSSIPKQRRVEGKSGRSSEHKSGSD 935

RESULT 8
US-07-814-964-11
; Sequence 11, Application US/07814964
; Patent No. 5359047
; GENERAL INFORMATION:
; APPLICANT: Donahue, Brian A.
; APPLICANT: Toney, Jeffrey H.
; APPLICANT: Bruhn, Suzanne L.
; APPLICANT: Pili, Pieter M.
; APPLICANT: Brown, Steven
; APPLICANT: Kellert, Patti
; APPLICANT: Essigmann, John M.
; APPLICANT: Lippard, Stephen J.
; TITLE OF INVENTION: DNA Structure Specific Recognition
; TITLE OF INVENTION: Protein and Uses Therefor
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: 2 Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
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; NAME/KEY: Domain
; LOCATION: 632..649
; OTHER INFORMATION: /label= Basic II
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 657..723
; OTHER INFORMATION: /label= Mixed Charge
US-08-258-442-11

Query Match
Best Local Similarity 5.9%; Score 135.5; DB 1; Length 723;
Matches 81; Conservative 37; Mismatches 114; Indels 117; Gaps 18;

Qy 126 DYLK-----HLKVKKIPSPFEGSGYTLQERGNDISPFSGDGPFFKIDPG-KGEATGPD 180
Db 416 DYITQKHLVSNMCK-----DKSGYKDV-DFGSD-----NENEPDAYLARLKAAREKE 464
Qy 181 LEGKDITQTFAGPSEAESETHLDTKKPGYNEIPREENGNTIGTRDETAKEDADVSLV 240
Db 465 EDDDD-----GDSDESTDEDF-KPNESEDVAEYDSNVESDSD-----DSDASG----- 510
Qy 241 EGSNDIMGSTNFKELPGREGNRVNDAQSONAHQGVFHYPPAPSKERKEGS----- 292
Db 511 -GGGSDGAKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 562
Qy 293 -----SDAAES-----TNYNEIPKNGKSTRGKGVDSHNRNQATLNKQRPSPKSGKSQL 341
Db 563 MLWINDTRESIKRENPGIKVTEIAKGGEMWKKELKDKSKWEDAAKDKQRY----- 613
Qy 342 PIPSRGLDNEIKNEMDSFNGPSHENIITHGRKXHYVPHRQNNSTRNKGMPQKSGWGR-- 399
Db 614 -----HDEMRYKPEAGGSDSNEKG-----GKSSKKRKT 642
Qy 400 QPHSNRR-----FSSRR--RDSSESSDSSGSSSE-----SDGD 430
Db 643 EPSPKKANTSGSGFKSKEYISDDSTSDDEKDNPAKKKPPSPGD 691

RESULT 11
US-08-328-809-6
; Sequence 6, Application US/08866840
; Patent No. 6475791
; GENERAL INFORMATION:
; APPLICANT: Lippard, Stephen J.
; APPLICANT: Essigmann, John M.
; APPLICANT: Donahue, Brian A.
; APPLICANT: Brown, Steven
; APPLICANT: Kelletr, Patti
; TITLE OF INVENTION: Uses For DNA Structure-Specific
; TITLE OF INVENTION: Recognition Proteins
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Patent Administrator, Testa, Hurwitz & Thibault
; STREET: 53 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,809
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fenton, Gillian M.
; REGISTRATION NUMBER: 36,508
```



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Query Match      5.9%; Score 135.5; DB 4; Length 723;
Best Local Similarity 23.2%; Pred. NO. 0.0032;
Matches 81; Conservative 37; Mismatches 114; Indels 117; Gaps 18;

QY    126 DYLK----HLKVKIKPISDFEGSYITDLOERGNDISPFSGDGQPKDIGP-KGEATGPD 180
       ||| .|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.
Db     416 DYTQKKLHVSNGK-----DKSGYKDV-DFGUSD-----NENEPPAYLARLKAEAREKE 464
       |||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.
QY    181 LESKDQTGTGAGSSEAESHTLDTPKKPGYNIEIPREENGNTTIGTRDETAKEADVDSLV 240
       :|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.

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; OTHER INFORMATION: /label= Acidic
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 518..547
; OTHER INFORMATION: /label= Basic I
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 547..620
; OTHER INFORMATION: /label= HMG-box
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 632..649
; OTHER INFORMATION: /label= Basic II
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 657..723
; OTHER INFORMATION: /label= Mixed Charge
PCT-US92-11107-11

Query Match      5.9%; Score 135.5; DB 5; Length 723;
Best Local Similarity 23.2%; Pred. No. 0.0032;
Matches 81; Conservative 37; Mismatches 114; Indels 117; Gaps 18;

QY 126 DYLK-----HLKVKKIPSDPFGSGYTLQBRGNDISPPFGDQGFQFIDFG-KGEATGPD 180
Db 416 DYITQKLLHVSNMKG-----DKSGYKDV-DFGDS-----NENEPDAYLARLKAEAREKE 464
QY 181 LEGKDIOGTGAGSEABSTHLDTKKPGYNEIPEREENGNTIGTRDTAKEADAVDSL 240
Db 465 EDDDD-----GSDSESTEDF-KPNESDVABEYDSVSDSD-----DSDASG----- 510
QY 241 EGSNDIMSTNFKELPREGNVDAGSQAHQGVPHYPPAPSKKKEKGS----- 292
Db 511 -GGSDGAKKKKKEKKEKKEKKEKKEK-----KPSKKKDGKPKRATTAF 562
QY 293 -----SAAES-----TNYNEIPKNGKSTRGVHNSNQATLNEKQFPKSGKSGQL 341
Db 563 MLWINDTRESIKRENFGIKVTEIAKGGEMWELKDKSKWEDAAAKDKQRY----- 613
QY 342 PIPSRGLDNEIKEMDSFNGSPSHENIITHGRKYHYVPHRQNNNTRNKGMPQKGSWGR-- 399
Db 614 -----HDMKNYKPEAGGSDNKEG-----GKSKKRKT 642
QY 400 QPHSNR-----FSSRR--RDDSESSDSGSSE-----SDGD 430
Db 643 EFSPPKKANTSGSGFKSKYISDDTSSDDEKDNPEAKKSPPSDGD 691

RESULT 13
US-08-568-459A-2
; Sequence 2, Application US/08568459A
; Patent No. 5849306
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/568,459A
; FILING DATE: 07-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelisen, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1115 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium vivax
; US-08-568-459A-2

Query Match      5.9%; Score 134.5; DB 2; Length 1115;
Best Local Similarity 20.0%; Pred. No. 0.0071;
Matches 97; Conservative 80; Mismatches 220; Indels 89; Gaps 21;

QY 2 NKEYSISNKENTHNLGRMSIYPKSTGNKGPEDGDADSLKLDQBEYGAALIRNMQHIMG 61
Db 500 NTFISVKNKAEKVOTAGIVPEY-----DILKQ--ELDEFNEVAFENIKRDG 544
QY 62 PVTAKLLG-EENKENTPRVLNIIIPASMYAKAHKSKDKKPPORDSOAQKSPVKSKSTHR 120
Db 545 AYIELCVCSVEEAKKNTQEVTVNVNNAKSOA-TNSNPISQPVDSKAEKVP--GDSTH- 600
QY 121 IQHNIDYLKHLKSV-KKIPSPDFEGSGYTDLQ---ERCDNDISPFSGDQGFQFIDFGKE- 175
Db 601 --GNVNSGQSSSTTGKAVTGDGQNGNQTPAESDVQRSDIAESVSAKNVDPQKSVSKRSD 658
QY 176 ---ATGPDLEGKDIQTGFAGPSEASTHLDTKKFG-----YNEI 211
Db 659 TASVTGIAEAGKE-NLGASNSRESEST-VEANSFGDDTVNSAIPVVGGENPLVTPFNGL 716
QY 212 PEREENGNN-----TIGTRDTAKEADAVDSLVEGSDNDIMGSTNFKELPREGN 261
Db 717 RHKONSDDGPAESMANPDSNSKGETGKQDNDMAKATKDSNSSSDGTS-----SATGD 771
QY 262 RVDAGSQAHQGVPHYPPAPSKKKEKGS---DAAESTNYNEIPKNGKST---RKG 315
Db 772 TTDADVREINKGVFEDRDKTVGSKDGGEDNSANKDAATVVGDRIRENSAGGSTNDRSK 831
QY 316 VHSNRNQATLNEKQR--FPKSGKSOGLPIPSRG--LDNEIKEMDSFNGSPSHENIITHG 371
Db 832 NUTKNGASTPDSKQSEDTALSKTESLESTESGDRITNDTNSLNKNGKGDQKQHD 891
QY 372 RYHYVPHRQNNSTR-----NKGMPQKSGWGRQPHSNR-RFSSRRRDDSESSDSG 422
Db 892 FKSNDTPNEEPSNDQTDAEGHDRDSIKNDKAE--RRKHMKNKDTFTKNTNSHLNNSNL 949
QY 423 SSESSED 428
Db 950 SNGKLD 955

RESULT 14
US-08-487-826B-2
; Sequence 2, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
```

APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellem, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israel, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1115 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Plasmodium vivax
US-08-487-826B-2
Query Match 5.9%; Score 134.5; DB 2; Length 1115;
Best Local Similarity 20.0%; Pred. No. 0.0071;
Matches 97; Conservative 80; Mismatches 220; Indels 89; Gaps 21;
QY 2 NKEYSISNKENTHGLRMSIYPSKTNKGFEDGDDAISKLHDOEYGAALIRNMQHIMG 61
Db 500 NKFSVKNAEKVQTAGIVTPY-----DILKQ--ELDEFNEVAFENEINKRDG 544
QY 62 PVTAKLLG-EENKENTPRVNLNIPASMYAKAHSKDKKKPQDSQAOKSPVKSSTHR 120
Db 545 AYELCVCSVEEAKKNTQEVVTVNDVNAKSAQA-TNSNPISQPVDSKAEKVP--GDSTH- 600
QY 121 IQHNIDYLKHLKSV-KKIPSPDFEGSGYTDLQ---ERGDNDISPFSGDGPFPKDPKGGE- 175
Db 601 --GNVNSGQDSSTTGKAVTGDGNGQNTPAESDVQSRDIAESVSAKNVDFQKSVKESDD 658
QY 176 ---ATGPDLEKGIQITGFAGPSEASTHLDTKPG-----YNEI 211
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QY 212 PEREENGNN-----TIGRDETAKADAVDSVLGSGNDIMGSTNFKELPGEGN 261
Db 717 RHSDKNSDGPASMANPDSNKGKGTGKQDNDMAKATKSSNSDGTG-----SATGD 771
QY 262 RVDAGSQNAHQGVFHYPPAPSKERKEGSS---DAAESTNYNEIPKNGKST---RKG 315
Db 772 TTDVADREINKGVPEDRDKTVGSKDGGEDNSANKDAATVVGEDRRENSAGSTNDRSK 831
QY 316 VDSHNRQATLNKQR--FPKSKSQGLPIPSRG--LDNEIRNEMDSFNGPSHENIITHG 371
Db 832 NDTKNGASTPDSKQSEDATALSKTESLSTESGSDRTTNDTNSLENKNGKGEKDIQKHD 891

QY 372 RKYHYVPHRONNSTR-----NKGMPQKSGWGRQPHNRR-RFSRRRDDSESDSG 422
Db 892 FKSGNDTPNEEPNSQTTDAEGHSDRDSIKNDKAE--RRKHNKDTFTKNTNSHLSNNL 949
QY 423 SSSESQ 428
Db 950 SNGKLD 955
RESULT 15
US-09-210-288-2
Sequence 2, Application US/09210288
Patent No. 6392026
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellem, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1115 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Plasmodium vivax
US-09-210-288-2
Query Match 5.9%; Score 134.5; DB 4; Length 1115;
Best Local Similarity 20.0%; Pred. No. 0.0071;
Matches 97; Conservative 80; Mismatches 220; Indels 89; Gaps 21;
QY 2 NKEYSISNKENTHGLRMSIYPSKTNKGFEDGDDAISKLHDOEYGAALIRNMQHIMG 61
Db 500 NKFSVKNAEKVQTAGIVTPY-----DILKQ--ELDEFNEVAFENEINKRDG 544
QY 62 PVTAKLLG-EENKENTPRVNLNIPASMYAKAHSKDKKKPQDSQAOKSPVKSSTHR 120
Db 545 AYELCVCSVEEAKKNTQEVVTVNDVNAKSAQA-TNSNPISQPVDSKAEKVP--GDSTH- 600
QY 121 IQHNIDYLKHLKSV-KKIPSPDFEGSGYTDLQ---ERGDNDISPFSGDGPFPKDPKGGE- 175
Db 601 --GNVNSGQDSSTTGKAVTGDGNGQNTPAESDVQSRDIAESVSAKNVDFQKSVKESDD 658

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QY 176 ---ATCPDLEGKDIQTGFAGPSEAEETHLDTKKPG-----YNEI 211
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QY 212 PEREENGGN-----TIGTRDETAKEADAVSVLVEGSNDIMGSTNFKELPGREGN 261
Db 717 RSHKNSDSDGPAESMANPDSNSKGTGKGQDNDAKATKDSNSSDGT-----SATGD 771
QY 262 RVDAGSONAQKVEHYPPAPSKERKEGSS---DAESTYNEIPKNGKGT---RKG 315
Db 772 TTDAVDREINKGVPEDRDKTVGSKDGGEDNSANKDAATVVGEDRIRENSAGGSTNDRSK 831
QY 316 VDHSNRNQATLNEKOR--FPSKKSQGLPIPSRG--LDNEIKNEMDSFNGSPSHENIITHG 371
Db 832 NTEKNGASTPDKQSEDATALSKESTESGDRTTNDTTNSLENKNGGKEKDLQKHD 891
QY 372 RKYHYVPHRQNNSTR-----NKGMPQKGSWGQPHSNR-RFSRRRDDSSSSDSG 422
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QY 423 SSESSED 428
Db 950 SNGKLD 955

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Search completed: November 26, 2003, 15:49:09
 Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 26, 2003, 15:48:08 ; Search time 37 Seconds
(without alignments)
2143.530 Million cell updates/sec

Title: US-09-700-696C-2
Perfect score: 2279
Sequence: 1 VNKEYSISNKENTHGLRMS.....RRDSSBSSDGSSESSEDGD 430

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 184443283 residues

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2276	99.9	509	12	US-09-794-422-34
2	2276	99.9	525	12	US-09-794-422-34
3	2276	99.9	525	12	US-09-794-422-6
4	2276	99.9	540	12	US-10-311-840-1
5	2276	99.9	540	12	US-09-794-422-46
6	2269	99.6	556	12	US-09-794-422-8
7	983.5	43.2	441	12	US-09-814-550-2
8	938.5	41.2	435	12	US-09-794-422-4
9	514	22.6	97	10	US-09-794-422-2
10	246	10.8	47	10	US-09-812-485A-1
11	235.5	10.3	47	10	US-09-812-485A-2
12	229	10.0	47	10	US-09-812-485A-3
13	218	9.6	40	10	US-09-812-485A-4
14	216	9.5	44	10	US-09-812-485A-23
15	215	9.4	44	10	US-09-812-485A-6

16	214.5	9.4	45	10	US-09-812-485A-27	Sequence 27, Appl
17	198.5	8.7	41	10	US-09-812-485A-8	Sequence 8, Appl
18	190.5	8.4	40	10	US-09-812-485A-24	Sequence 24, Appl
19	188.5	8.3	40	10	US-09-812-485A-32	Sequence 32, Appl
20	182	8.0	37	10	US-09-812-485A-7	Sequence 7, Appl
21	180	7.9	38	10	US-09-812-485A-10	Sequence 10, Appl
22	163.5	7.2	35	10	US-09-812-485A-25	Sequence 25, Appl
23	157.5	6.9	35	10	US-09-812-485A-28	Sequence 28, Appl
24	153.5	6.7	33	10	US-09-812-485A-30	Sequence 30, Appl
25	152	6.7	1253	12	US-10-363-798-2	Sequence 2, Appl
26	150	6.6	32	10	US-09-812-485A-12	Sequence 12, Appl
27	148	6.5	1884	10	US-09-785-770A-17	Sequence 17, Appl
28	148	6.5	1907	10	US-09-785-770A-16	Sequence 16, Appl
29	146.5	6.4	33	10	US-09-812-485A-31	Sequence 31, Appl
30	146	6.4	2174	12	US-10-087-887-87	Sequence 87, Appl
31	144.5	6.3	665	11	US-09-820-843A-107	Sequence 107, Appl
32	142.5	6.3	31	10	US-09-812-485A-33	Sequence 33, Appl
33	142.5	6.3	31	10	US-09-812-485A-36	Sequence 36, Appl
34	140	6.1	772	15	US-10-153-668-302	Sequence 302, Appl
35	137.5	6.0	30	10	US-09-812-485A-26	Sequence 26, Appl
36	136	6.0	1210	15	US-10-205-823-264	Sequence 264, Appl
37	134.5	5.9	1115	14	US-10-153-273-2	Sequence 2, Appl
38	133.5	5.9	1462	12	US-10-287-218-17	Sequence 17, Appl
39	131.5	5.8	2476	11	US-09-824-574-7	Sequence 7, Appl
40	129.5	5.7	30	10	US-09-812-485A-29	Sequence 29, Appl
41	129.5	5.7	677	15	US-10-060-036-4552	Sequence 4552, Ap
42	129	5.7	28	10	US-09-812-485A-14	Sequence 14, Appl
43	127	5.6	322	11	US-09-746-660A-64	Sequence 64, Appl
44	127	5.6	718	10	US-09-738-626-5661	Sequence 5661, Ap
45	127	5.6	1365	11	US-09-884-465A-382	Sequence 382, Appl

ALIGNMENTS

RESULT 1

US-09-794-422-34
; Sequence 34, Application US/09794422
; Publication No. US20030165239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794, 422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 34
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-422-34

Query Match 99.9%; Score 2276; DB 12; Length 509;
Best Local Similarity 99.8%; Pred. No. 4.3e-173;
Matches 429; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	VNKEYSISNKENTHGLRMSIYKSTGNGKGFEGDDAISKLHPQEEYGAALIRNNQHM	60
Db	80	LNKEYSISNKENTHGLRMSIYKSTGNGKGFEGDDAISKLHPQEEYGAALIRNNQHM	139
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Db	140	GPVTAIKLLGEENKENTPRNLNIIIPASMYAKAHSKDKKKPQDSQAOKSPVKSKSTHR	199
QY	121	IQHNIDYKHLKSKVKKIPSDFGSGYTDLQERGDNDISPFSGDGQPPKDIKPGKEATGPD	180

Db 200 IQHNIDYLVKHLKSVKVKIPSPDEFGSGYTDLQERGDNDISPFSGDQPPKDIIPKGGEATGPD 259
Qy 181 LEGKDIQTGFAGPSEAEASTHLDTKKPGYNEIPEEREENGNTIGTRDETAKADAVDVSLV 240
Db 260 LEGKDIQTGFAGPSEAEASTHLDTKKPGYNEIPEEREENGNTIGTRDETAKADAVDVSLV 319
Qy 241 EGSNDIMGSTNFKELPGREGNRVDAGSQNAHQGVFHYPPAPSKERKEGSSDAAEASTN 300
Db 320 EGSNDIMGSTNFKELPGREGNRVDAGSQNAHQGVFHYPPAPSKERKEGSSDAAEASTN 379
Qy 301 YNEIPKNGKSTRKGVVPHRQNNSTRNKGMPQKGSWGRQPHSNRRFSSRRRDDSSSD 360
Db 380 YNEIPKNGKSTRKGVVPHRQNNSTRNKGMPQKGSWGRQPHSNRRFSSRRRDDSSSD 439
Qy 361 GPSHENIITHGRKYHYVPHRQNNSTRNKGMPQKGSWGRQPHSNRRFSSRRRDDSSSD 420
Db 440 GPSHENIITHGRKYHYVPHRQNNSTRNKGMPQKGSWGRQPHSNRRFSSRRRDDSSSD 499
Qy 421 SGSSSESDDG 430
Db 500 SGSSSESDDG 509

RESULT 2

US-09-794-422-6

; Sequence 6, Application US/09794422

; Publication No. US20030166239A1

; GENERAL INFORMATION:

; APPLICANT: Brown, Thomas A.

; APPLICANT: De Wet, Jeffrey R.

; APPLICANT: Gowen, Lori C.

; APPLICANT: Hames, Lynn M.

; TITLE OF INVENTION: Mammalian Osteoregulins

; FILE REFERENCE: PC10445

; CURRENT APPLICATION NUMBER: US/09/794,422

; CURRENT FILING DATE: 2001-02-27

; PRIOR FILING DATE: 60/185,617

; PRIOR FILING DATE: 2000-02-29

; PRIOR FILING DATE: 60/234,500

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 6

; LENGTH: 525

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-794-422-6

Query Match 99.9%; Score 2276; DB 12; Length 525;
Best Local Similarity 99.8%; Pred. No. 4.5e-173;
Matches 429; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNKEYSISNKTNGHGLRMSIYPKSTGNKGFGDDAISKLDHDEYGAALIRNMQHIM 60
Db 96 LNKEYSISNKTNGHGLRMSIYPKSTGNKGFGDDAISKLDHDEYGAALIRNMQHIM 155
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Qy 121 IQHNIDYLVKHLKSVKVKIPSPDEFGSGYTDLQERGDNDISPFSGDQPPKDIIPKGGEATGPD 180
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Qy 241 EGSNDIMGSTNFKELPGREGNRVDAGSQNAHQGVFHYPPAPSKERKEGSSDAAEASTN 300
Db 336 EGSNDIMGSTNFKELPGREGNRVDAGSQNAHQGVFHYPPAPSKERKEGSSDAAEASTN 395

Qy 301 YNEIPKNGKSTRKGVVPHRQNNSTRNKGMPQKGSWGRQPHSNRRFSSRRRDDSSSD 360
Db 396 YNEIPKNGKSTRKGVVPHRQNNSTRNKGMPQKGSWGRQPHSNRRFSSRRRDDSSSD 455
Qy 361 GPSHENIITHGRKYHYVPHRQNNSTRNKGMPQKGSWGRQPHSNRRFSSRRRDDSSSD 420
Db 456 GPSHENIITHGRKYHYVPHRQNNSTRNKGMPQKGSWGRQPHSNRRFSSRRRDDSSSD 515
Qy 421 SGSSSESDDG 430
Db 516 SGSSSESDDG 525

RESULT 3

US-10-311-840-1

; Sequence 1, Application US/10311840

; Publication No. US20030175808A1

; GENERAL INFORMATION:

; APPLICANT: KUROKAWA, Tomofumi

; APPLICANT: YAMADA, Takao

; APPLICANT: MORIMOTO, Shigeto

; TITLE OF INVENTION: No. US20030175808A1el Protein and its DNA

; FILE REFERENCE: 2738USOP

; CURRENT APPLICATION NUMBER: US/10/311,840

; CURRENT FILING DATE: 2002-12-18

; PRIOR APPLICATION NUMBER: PCT/JP01/05263

; PRIOR FILING DATE: 2001-06-20

; PRIOR APPLICATION NUMBER: JP 2000-191088

; PRIOR FILING DATE: 2000-06-21

; NUMBER OF SEQ ID NOS: 10

; SEQ ID NO 1

; LENGTH: 525

; TYPE: PRT

; ORGANISM: Human

; US-10-311-840-1

Query Match 99.9%; Score 2276; DB 12; Length 525;
Best Local Similarity 99.8%; Pred. No. 4.5e-173;
Matches 429; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNKEYSISNKTNGHGLRMSIYPKSTGNKGFGDDAISKLDHDEYGAALIRNMQHIM 60
Db 96 LNKEYSISNKTNGHGLRMSIYPKSTGNKGFGDDAISKLDHDEYGAALIRNMQHIM 155
Qy 61 GPVTAIKLGEENKENTPRNVNLIIPASMYAKAHSKDKKKPQDSDQAQKSPVKSKSTHR 120
Db 156 GPVTAIKLGEENKENTPRNVNLIIPASMYAKAHSKDKKKPQDSDQAQKSPVKSKSTHR 215
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Qy 181 LEGKDIQTGFAGPSEAEASTHLDTKKPGYNEIPEEREENGNTIGTRDETAKADAVDVSLV 240
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Db 516 SGSSSESDDG 525

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RESULT 4
US-09-794-422-46
; Sequence 46, Application US/09794422
; Publication No. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-422-46

Query Match          99.9%; Score 2276; DB 12; Length 540;
Best Local Similarity 99.8%; Pred. No. 4.7e-173;
Matches 429; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 111 LNKEYSISNKENTHNGLRMSIYPKSTGNKGFEQDDAISKLHQEYGAALIRNNQHM 170
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Db 231 IQHNIDYLKHLKSVKKIPSPDFEGSGYTDLQERGNDISPFSGDGQPKDIPGKEATGPD 290
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QY 241 EGSNDIMGSTNFKELPREGNVDAGSNQATLNKQRPFSKGSQGLPIPSRGLDNEIKNEMDSFN 300
Db 351 EGSNDIMGSTNFKELPREGNVDAGSNQATLNKQRPFSKGSQGLPIPSRGLDNEIKNEMDSFN 410
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Db 411 YNEIPKNGKSTRKGVDSHNRNQTALNKKQRPFSKGSQGLPIPSRGLDNEIKNEMDSFN 470
QY 361 GFSHENIITHGRKYHYVPHRQNNSTNKGMPQKGSWGRPHSNRRFSSRRDDSSSSD 420
Db 471 GFSHENIITHGRKYHYVPHRQNNSTNKGMPQKGSWGRPHSNRRFSSRRDDSSSSD 530
QY 421 SGSSSESDDG 430
Db 531 SGSSSESDDG 540

RESULT 5
US-09-794-422-8
; Sequence 8, Application US/09794422
; Publication No. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445

```

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; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-422-8

Query Match          99.9%; Score 2276; DB 12; Length 556;
Best Local Similarity 99.8%; Pred. No. 4.9e-173;
Matches 429; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNKEYSISNKENTHNGLRMSIYPKSTGNKGFEQDDAISKLHQEYGAALIRNNQHM 60
Db 127 LNKEYSISNKENTHNGLRMSIYPKSTGNKGFEQDDAISKLHQEYGAALIRNNQHM 186
QY 61 GPTVAILKLGEEKENTPRNLNIIIPASMYAKAHSKDKKKPORDSQAKSPVKSKSTHR 120
Db 187 GPTVAILKLGEEKENTPRNLNIIIPASMYAKAHSKDKKKPORDSQAKSPVKSKSTHR 246
QY 121 IQHNIDYLKHLKSVKKIPSPDFEGSGYTDLQERGNDISPFSGDGQPKDIPGKEATGPD 180
Db 247 IQHNIDYLKHLKSVKKIPSPDFEGSGYTDLQERGNDISPFSGDGQPKDIPGKEATGPD 306
QY 181 LEGKDIQTGFAGPSEASTHLDTKPKGYNEIPREENGNTIGTRDETAKADAVDSL 240
Db 307 LEGKDIQTGFAGPSEASTHLDTKPKGYNEIPREENGNTIGTRDETAKADAVDSL 366
QY 241 EGSNDIMGSTNFKELPREGNVDAGSNQATLNKQRPFSKGSQGLPIPSRGLDNEIKNEMDSFN 300
Db 367 EGSNDIMGSTNFKELPREGNVDAGSNQATLNKQRPFSKGSQGLPIPSRGLDNEIKNEMDSFN 426
QY 301 YNEIPKNGKSTRKGVDSHNRNQTALNKKQRPFSKGSQGLPIPSRGLDNEIKNEMDSFN 360
Db 427 YNEIPKNGKSTRKGVDSHNRNQTALNKKQRPFSKGSQGLPIPSRGLDNEIKNEMDSFN 486
QY 361 GFSHENIITHGRKYHYVPHRQNNSTNKGMPQKGSWGRPHSNRRFSSRRDDSSSSD 420
Db 487 GFSHENIITHGRKYHYVPHRQNNSTNKGMPQKGSWGRPHSNRRFSSRRDDSSSSD 546
QY 421 SGSSSESDDG 430
Db 547 SGSSSESDDG 556

RESULT 6
US-09-814-550-2
; Sequence 2, Application US/09814550
; Patent No. US20020102641A1
; GENERAL INFORMATION:
; APPLICANT: Schiavi, Susan
; APPLICANT: Madden, Stephen
; APPLICANT: Manavalan, Parthasarathy
; APPLICANT: Levine, Michael
; APPLICANT: Jan de Beur, Suzanne
; TITLE OF INVENTION: ONCOGENIC OSTEOMALACIA-RELATED GENE 1
; FILE REFERENCE: 5014US
; CURRENT APPLICATION NUMBER: US/09/814,550
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/191,786
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/241,598
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 525

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/ TYPE: PRT
; ORGANISM: Homo sapiens
US-09-814-550-2

Query Match          99.6%; Score 2269; DB 10; Length 525;
Best Local Similarity 99.5%; Pred. No. 1.6e-172;
Matches 428; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VNKEYSINKENTHNGLRMSIYPKSTGNKGFEDGDDAISKLHDOBEYGAALIRNNQHIM 60
Db LNKEYSINKENTHNGLRMSIYPKSTGNKGFEDGDDAISKLHDOBEYGAALIRNNQHIM 155
QY 61 GPVTATKLLGEENKENTPRNVLIIPASMYAKAHSKDKKKPQDSQAQKSPVKS 120
Db GPVTATKLLGEENKENTPRNVLIIPASMYAKAHSKDKKKPQDSQAQKSPVKS 120
QY 156 GPVTATKLLGEENKENTPRNVLIIPASMYAKAHSKDKKKPQDSQAQKSPVKS 215
Db GPVTATKLLGEENKENTPRNVLIIPASMYAKAHSKDKKKPQDSQAQKSPVKS 215
QY 121 IQHNIDYLKHLKSVKVIIPSDFEKGYTDLQERGNNDISPFSGDQPPKIPGKEATGPD 180
Db IQHNIDYLKHLKSVKVIIPSDFEKGYTDLQERGNNDISPFSGDQPPKIPGKEATGPD 275
QY 216 IQHNIDYLKHLKSVKVIIPSDFEKGYTDLQERGNNDISPFSGDQPPKIPGKEATGPD 240
Db IQHNIDYLKHLKSVKVIIPSDFEKGYTDLQERGNNDISPFSGDQPPKIPGKEATGPD 275
QY 181 LEGKDIQTGFAGPSEABSTHLDTKKPGYNEIPEREENGNTIGTRDETAKADAVDVSLV 360
Db LEGKDIQTGFAGPSEABSTHLDTKKPGYNEIPEREENGNTIGTRDETAKADAVDVSLV 335
QY 241 EGSNDIMGSTNFELPGREGNRYDAGSONAHQGVKVEFHYPPAPSKKKEGSSDAABSTN 300
Db EGSNDIMGSTNFELPGREGNRYDAGSONAHQGVKVEFHYPPAPSKKKEGSSDAABSTN 395
QY 301 YNEIPKNGKSTRKGVDSHNRNQTALNEKORFPSPKSGKSGQLPIPSRGLDNEIKNEMDSFN 360
Db YNEIPKNGKSTRKGVDSHNRNQTALNEKORFPSPKSGKSGQLPIPSRGLDNEIKNEMDSFN 455
QY 361 GPSHENIITHGRKYHYVPHRQNNSTRNKGMPQKGSGWGRQPHNRRPSSRRDDSSSSD 420
Db GPSHENIITHGRKYHYVPHRQNNSTRNKGMPQKGSGWGRQPHNRRPSSRRDDSSSSD 515
QY 421 SGSSSESDDG 430
Db SGSSSESDDG 525

RESULT 7
US-09-794-422-4
; Sequence 4, Application US/09794422
; Publication No. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-794-422-4

Query Match          43.2%; Score 983.5; DB 12; Length 441;
Best Local Similarity 50.5%; Pred. No. 3.6e-70;
Matches 217; Conservative 52; Mismatches 134; Indels 27; Gaps 8;

QY 6 SINKENTHNGLRMSIYPKSTGNKGFEDGDDAISKLHDOBEYGAALIRNNQHIMGPVTA 65
Db SCGNODSIHKLDAASYVDPDTEDEGTGQALLHPGQDRYGAALIRNITQPVKSLVTG 93

Query Match          41.2%; Score 938.5; DB 12; Length 435;
Best Local Similarity 49.4%; Pred. No. 1.4e-66;
Matches 211; Conservative 45; Mismatches 146; Indels 25; Gaps 8;

QY 9 NKENTHNGLRMSIYPKSTGNKGFEDGDDAISKLHDOBEYGAALIRNNQHIMGPVTA 68
Db NQGNTH---LASVKPEPMVKGTGGGRDAPLHLLDQNRQATLLRNITQPVKSLVTGTEV 85
QY 69 LGEENKENTPRNVLIIPASMYAKAHSKDKKKPQDSQAQKSPVKSSTHRIQHIDYL 128
Db QSDRNEKKKPPQSVLSVIPDVTNNTDYSEDTEQQRDLLONSPGQSKHTPRARRSTHYL 145
QY 129 KHLKSVKVIIPSDFEKGYTDLQERGNNDISPFSGDQPPKIPGKEATGPDLE---GKD 185
Db THLPQIRKILSLDFEDSASPDLLVRGNDVPPFSGDQGHFWHTPDRGAVGSDPESSAGHP 205
QY 186 IQTGFAGPSEABSTHLDTKKPGYNEIPEREENGNTIGTRDETAKADAVDVSLV 245
Db IQTGFAGPSEABSTHLDTKKPGYNEIPEREENGNTIGTRDETAKADAVDVSLV 245
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Db 206 V----SGSSNVEIVDPHTNGLSGNEIPGREGHIGGAYATRGKTAQAGSADYSLVEGSNE 261
QY 246 IMGSTNEXELPCREGNRYVDAGSONAHQGVVEHYPPAPSKERKKGSSDAESTYNYNEIP 305
Db 262 ITGSTKFLPEKGNRYVDASSQNAHQGVVEHYPPAPSKERKKGSSREHTKAGYNEIP 321
QY 306 KMGKSTRKGVDPHSNRNQATLNEKORFPSPKSKSGQLPIPSRGLDNEIKNEMDSFNGPSHE 365
Db 322 KSKGKASKDAESKGNQVTLTESQRFPGKGGQS-----SHSLGNEVKSEEDSSNSLSRE 377
QY 366 NI-ITHGRKYHVPHRONNNTKMGPKQKSW-GRQPHSNRRFSSRRDDSSSDSGS 423
Db 378 GIAIAHRRTSH-----PTRNRGMSQRSGSWARRPHPRRVSTRQR-DSSESSSGS 428
QY 424 SSESQGD 430
Db 429 SSESQGD 435

RESULT 9
US-09-812-485A-1
; Sequence 1, Application US/09812485A
; Publication No. US20020197267A1
; GENERAL INFORMATION:
; APPLICANT: Kumagai, Yoshinari
; APPLICANT: Blacher, Russel
; APPLICANT: Yoneda, Toshiyuki
; TITLE OF INVENTION: Integrin Binding Motif Containing
; TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases
; FILE REFERENCE: BEAR-006CIP
; CURRENT APPLICATION NUMBER: US/09/812,485A
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/641,034
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptidic compound
US-09-812-485A-1

Query Match 22.6%; Score 514; DB 10; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.2e-33;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 DSQAQSPVKSKSTHRIQHNIDYKHLKSKVKKIPSPDFGSGYTDLQERGDNDISPFSGDG 164
Db 1 DSQAQSPVKSKSTHRIQHNIDYKHLKSKVKKIPSPDFGSGYTDLQERGDNDISPFSGDG 60
QY 165 QPFKDIQKGEATGPDLEKDIQTGFAGPSEASTHL 201
Db 61 QPFKDIQKGEATGPDLEKDIQTGFAGPSEASTHL 97

RESULT 10
US-09-812-485A-2
; Sequence 2, Application US/09812485A
; Publication No. US20020197267A1
; GENERAL INFORMATION:
; APPLICANT: Kumagai, Yoshinari
; APPLICANT: Blacher, Russel
; APPLICANT: Yoneda, Toshiyuki
; TITLE OF INVENTION: Integrin Binding Motif Containing
; TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases
; FILE REFERENCE: BEAR-006CIP
; CURRENT APPLICATION NUMBER: US/09/812,485A
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/641,034
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 50
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptidic compound
US-09-812-485A-2

Query Match 10.8%; Score 246; DB 10; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 AQKSPVKSKSTHRIQHNIDYKHLKSKVKKIPSPDFGSGYTDLQERGD 154
Db 1 AQKSPVKSKSTHRIQHNIDYKHLKSKVKKIPSPDFGSGYTDLQERGD 47

RESULT 11
US-09-812-485A-4
; Sequence 4, Application US/09812485A
; Publication No. US20020197267A1
; GENERAL INFORMATION:
; APPLICANT: Kumagai, Yoshinari
; APPLICANT: Blacher, Russel
; APPLICANT: Yoneda, Toshiyuki
; TITLE OF INVENTION: Integrin Binding Motif Containing
; TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases
; FILE REFERENCE: BEAR-006CIP
; CURRENT APPLICATION NUMBER: US/09/812,485A
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/641,034
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptidic compound
US-09-812-485A-4

Query Match 10.3%; Score 235.5; DB 10; Length 47;
Best Local Similarity 94.0%; Pred. No. 7.3e-12;
Matches 47; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 105 DSQAQSPVKSKSTHRIQHNIDYKHLKSKVKKIPSPDFGSGYTDLQERGD 154
Db 1 DSQAQSPVKSKSTHRIQHNIDYKHLKSKVKKIPSPDFGSGYTD--RGD 47

RESULT 12
US-09-812-485A-3
; Sequence 3, Application US/09812485A
; Publication No. US20020197267A1
; GENERAL INFORMATION:
; APPLICANT: Kumagai, Yoshinari
; APPLICANT: Blacher, Russel
; APPLICANT: Yoneda, Toshiyuki
; TITLE OF INVENTION: Integrin Binding Motif Containing
; TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases
; FILE REFERENCE: BEAR-006CIP
; CURRENT APPLICATION NUMBER: US/09/812,485A
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/641,034
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Artificial Sequence
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Search completed: November 26, 2003, 15:53:39
Job time : 38 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 29, 2003, 22:43:06 ; Search time 83 Seconds
(without alignments)
2286.684 Million cell updates/sec

Title: US-09-700-696C-2

Perfect score: 2279

Sequence: 1 VNKEYSISNKENHNGHRLMS.....RRDSSBSDSGSSSDGD 430

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=issued Patents NA -QFMT=fastaf -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	150	6.6	6755	3	US-08-931-999-4
2	140	6.1	2690	1	US-08-524-757-11
3	138.5	6.1	2384	1	US-07-814-964-10
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5	138.5	6.1	2384	1	US-08-328-809-5
6	138.5	6.1	2384	1	US-08-866-840-5
7	138.5	6.1	2384	5	PCT-US92-11107-10
8	137	6.0	9370	1	US-08-320-559-27
9	137	6.0	9370	3	US-08-545-860D-27
10	137	6.0	9370	5	PCT-US94-04496-27
11	137	6.0	9391	1	US-08-320-559-25
12	137	6.0	9391	3	US-08-545-860D-25

13	137	6.0	9391	5	PCT-US94-04496-25
14	134.5	5.9	4084	2	US-08-568-459A-1
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16	134.5	5.9	4084	4	US-09-210-288-1
17	134.5	5.9	4084	6	5198347-5
18	129	5.7	3157	6	5198347-3
19	127.5	5.6	3707	1	US-08-118-101A-1
20	127	5.6	2695	4	US-09-706-197-3
21	127	5.6	4215	4	US-09-620-312D-295
22	126.5	5.6	1393	5	PCT-US93-07261-12
23	126.5	5.6	3773	3	US-09-130-242-1
24	125.5	5.5	3825	3	US-09-208-742-3
25	125.5	5.5	5173	4	US-08-801-308-2
26	124.5	5.5	3552	4	US-09-134-001C-693
27	123	5.4	1503	3	US-08-999-774A-11
28	123	5.4	3534	4	US-09-134-001C-2269
29	123	5.4	4766	5	PCT-US93-07261-10
30	123	5.4	6775	4	US-09-620-312D-289
31	122.5	5.4	3347	4	US-09-702-705-318
32	122.5	5.4	3347	4	US-09-736-457-318
33	122	5.4	2073	4	US-09-134-001C-1731
34	122	5.4	43280	2	US-08-804-227C-1
35	121	5.3	2004	1	US-08-471-033-18
36	121	5.3	2004	2	US-08-471-044-18
37	121	5.3	2004	2	US-08-463-483A-18
38	121	5.3	2004	2	US-08-471-046A-18
39	121	5.3	2004	2	US-08-470-566B-18
40	121	5.3	2004	2	US-08-469-334-18
41	121	5.3	2004	3	US-09-300-529-18
42	121	5.3	2655	1	US-08-471-033-17
43	121	5.3	2655	2	US-08-471-044-17
44	121	5.3	2655	2	US-08-463-483A-17
45	121	5.3	2655	2	US-08-471-046A-17

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ALIGNMENTS

RESULT 1

US-08-931-999-4
; Sequence 4, Application US/08931999
; Patent No. 6043219
; GENERAL INFORMATION:
; APPLICANT: Iandolo, John J.
; TITLE OF INVENTION: Broad Spectrum Chemotherapeutic Peptide
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/931,999
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/710,561
; FILING DATE: 19-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 25043-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816/474-9050
; TELEFAX: 816/474-9057
; INFORMATION FOR SEQ ID NO: 4:


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; COUNTRY: US
; ZIP: 75270-2197
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/524,757
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13621
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160087
; FILING DATE: 30-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Harre, John A.
; REGISTRATION NUMBER: 37,345
; REFERENCE/DOCKET NUMBER: B35006C1PCIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (214) 939-4500
; TELEFAX: (214) 939-4600
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2690 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 33..2351
; US-08-524-757-11

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Alignment Scores:

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Pred. No.: 0.00039 Length: 2690
Score: 140.00 Matches: 87
Percent Similarity: 32.08% Conservative: 49
Best Local Similarity: 20.52% Mismatches: 144
Query Match: 6.14% Indels: 144
DB: 1 Gaps: 17

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US-09-700-696c-2 (1-430) x US-08-524-757-11 (1-2690)

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QY 43 AspGlnGluTyrGlyAlaAlaLeuIleArgAsnAsnMetGlnHisIleMetGlyPro 62
DB 720 CTGGTGACCCCATGGGAAGGGGTTGTGAGTCAAAACAGGAGCAC----- 767
QY 63 ValThrAlaIleLysLeuLeuGlyGluAsnLysGluAsnThrProArgAsnValLeu 82
DB 767 ----- 767
QY 83 AsnIleProLaserMetAsnTyrAlaLysAlaHisSerLysAspLysLysPro 102
DB 768 -----AAATCTTCCCAAGGACAAACGCCCGCTG 797
QY 103 GlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArgIleGln 122
DB 798 GATGCCAGAGTGATGAGAGGGCTCTGTGTGAGCAGAGAGAAATCACAC----- 848
QY 123 HisAsnIleAspTyrLeuLysHisLeuSerLysValLysLysIleProSerAspPheGlu 142
DB 849 -----AAGGCCCTCTCAAA----- 863
QY 143 GlySerGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspLysSerProPheSerGly 162
DB 864 -----GAGGAGAACCGAGGCCACCTTCAGGG 890

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QY 163 AspGlyGlnProPheLysAspIleProGlyLysGlyGluAlaThrGlyProAspLeuGlu 182
DB 891 GACAATGCAGGGAGAAACCG---CCCTCTAGTCGCTAAAGAAAGACAGACAGAGAG 947
QY 183 GlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSer---ThrHisLeu 201
DB 948 GGCAGCAGCCTGAAGAAGAAAGTGTTCCTCCCTCAGAGGCGCTTCAGAACACACCTG 1007
QY 202 AspThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsnThr 221
DB 1008 -----AAAAAGCCAAAGCACAGAGAC---CCAGAGAAAGCCAAA----- 1043
QY 222 IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValSerLeuValGlu 241
DB 1044 -----TTGGACAAAAGCAAGAGTCTGGACAGACTTGCACACAGGA-----AAA 1088
QY 242 GlySerAsnAspIleMet-----GlySerThrAsnPheLysGluLeu 255
DB 1089 GGAGCAGGAGACCTGTTGCCCAAGTAAAGAGAGAGGGTTCTTAACACCTAAAGACTCCA 1148
QY 256 ProGlyArgGluGlyAsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysVal 275
DB 1149 GAGGGAAAGTCAAAACTAATTGGATAGAAAGTCACTGGGCTCC---CTCCCTAAAGTT 1205
QY 276 -----GluPheHisTyrPro----- 280
DB 1206 GAGGAGACAGATATGAGAGATGAATTCGAGCAGCAACCATGTCTTTTGAATCTTACCTC 1265
QY 281 -----ProAlaProSerLysGluLysArgLysGluGlySerSerAspAlaGluSer 298
DB 1266 AGTATGACCAAGGCGGAGAGAAAGAAAGAAAGTGTGAAAAGT---TCAGCCACGGCA 1322
QY 299 ThrAsnTyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHis 318
DB 1323 CTGGAGATAAAGGACTTAAAAAATGACTCTAAAGACACTGGTAAAAAAGTGGACTCA 1382
QY 319 SerAsnArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSer 338
DB 1383 GTTCAGAAATATCCCAAGGTGAACAAACCAAGTCAGAGAAGCGGCTGGAGCTGATTTA 1442
QY 339 GlnGlyLeu----- 341
DB 1443 GCCAAGCTGAGAAAGGTGCTGATGTTCAGTGTTCAGACACTCCCGTTACCCGCG 1502
QY 342 -----ProIleProSerArgGlyLeuAspAsnGluIleLysAsnGlu 355
DB 1503 ATACAGGCCAATTACCGTCCACTGCTTCCCTCGAGCTGATATCTCTCTCCAGCCAAAG 1562
QY 356 MetAspSerPheAsnGlyProSerHisGluAsn----- 366
DB 1563 CGAAAAGCGTTCTTTCACCCAGGAAGAAAGAGCTGGATTTACTGGCGCAGAGATG 1622
QY 367 -----IleIleThrHisGlyArgLysTyrHisTyrValPro----- 378
DB 1623 AATTCCAAGATGAGGTGATTTCTGTTCCCAAGTGTGCTATCTCCCTAAAAATGATGACC 1682
QY 379 ---HisArgGln 381
DB 1683 TTGCACCAGCAA 1694

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RESULT 3

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US-07-814-964-10
; Sequence 10, Application US/07814964
; Patent No. 5359047
; GENERAL INFORMATION:
; APPLICANT: Donahue, Brian A.
; APPLICANT: Toney, Jeffrey H.
; APPLICANT: Bruhn, Suzanne L.
; APPLICANT: Pil, Pieter M.
; APPLICANT: Brown, Steven
; APPLICANT: Kellett, Patti
; APPLICANT: Essigmann, John M.

```

; APPLICANT: Lipbard, Stephen J.
 ; TITLE OF INVENTION: DNA Structure Specific Recognition
 ; TITLE OF INVENTION: Protein and Uses Therefor
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
 ; STREET: 2 Militia Drive
 ; CITY: Lexington
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02173
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/814,964
 ; FILING DATE: 19911226
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/539,906
 ; FILING DATE: 18-JUN-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Granahan, Patricia
 ; REGISTRATION NUMBER: 32,227
 ; REFERENCE/DOCKET NUMBER: MIT-4787AAA
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-861-6240
 ; TELEFAX: 617-861-9540
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2384 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; ORGANISM: Drosophila melanogaster
 ; IMMEDIATE SOURCE:
 ; CLONE: Drosophila SSRP - composite sequence
 ; POSITION IN GENOME:
 ; CHROMOSOME/SEGMENT: 2
 ; MAP POSITION: 60A 1-4
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 123..2291
 ; US-07-814-964-10

Alignment Scores:
 Pred. No.: 0.000459 Length: 2384
 Score: 138.50 Matches: 99
 Percent Similarity: 31.91% Conservative: 50
 Best Local Similarity: 21.20% Mismatches: 136
 Query Match: 6.08% Indels: 182
 DB: 1 Gaps: 23

US-09-700-696C-2 (1-430) x US-07-814-964-10 (1-2384)

Db	1341	-----GAGAGAGGAGGAG-----	1352
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Db	1353	-----TATGCCAAGCTC-----	1364
Qy	108	aGlnLysSerProValLysSerLysSerThrHisArgIleGlnHisAsnIleAspTyrIle	128
Db	1365	-----TTGCACTACAT	1375
Qy	128	uLys-----HisLeuSerLysValLysIleProSerAspPheGluGlySe	144
Db	1376	CACACAGAGAGAGTTCATGTCAGCAACATGGGCAAG-----GACAAGAG	1420
Qy	144	rGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspG1	164
Db	1421	CGGCTACAAGGACGTG--GACTTTGGTATTCCGAC-----AACGAGNA	1462
Qy	164	yGlnProPheLysAspIleProGly---LysGlyGluAlaThrGlyProAspLeuGluG1	183
Db	1463	CGAACACGATCCCTATCTGGCTCGCTCAGGCTGAGCGGAGGAGGAGGAGGACGA	1522
Qy	183	yLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAspTh	203
Db	1523	CGACGAT-----GGCGACTCGATGAGAGATCCACGATGAGGACTT	1564
Qy	203	rLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsnThrIleG1	223
Db	1565	C--AAGCCCAACGAGACGAGTCCGATGTCGCCGAGGAGTATGACACACGTCGAGAG	1621
Qy	223	yThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGluGlySe	243
Db	1622	TGATTCGACGAT-----GACAGCGATGCTAGTGGC-----GGCGG	1657
Qy	243	rAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGlyAsnArgVa	263
Db	1658	AGGCGACAGCGCGCGCCCAAGAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1717
Qy	263	lAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrProAlaPr	283
Db	1718	GGAGAAAAACACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1756
Qy	283	oSerLysGluLysArgLysGluGlySer-----AAACC	1756
Db	1757	CTCCAAG	1816
Qy	293	---SerAspAlaAlaGluSer-----ThrAsnTyrAsnGluI1	304
Db	1817	GCTGACGACACGCGCGAGAGATCAAGAGGAGAGAGAGAGAGAGAGAGAGAGAG	1876
Qy	304	eProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsnArgAsnGlnAl	324
Db	1877	CGCCAAGAGAGCGCGCGAGATGTGGAAGAGAGCTGAAGACAAAGTCCAAGTGGAGGATGC	1936
Qy	324	aThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGlyLeuProIlePr	344
Db	1937	GGCGGCCAAGGACCAAGCGCGCTAC-----	1961
Qy	344	oSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsnGlyProSerHi	364
Db	1961	-----	1961
Qy	364	sGluAsnIleIleThrHisGlyArgLysTyrHisTyrValProHisArgGlnAsnAsnSe	384
Db	1962	-----CACGACGAGATGCCCACTACAGCTCAAGCGCGCGGTGACAG	2005
Qy	384	rThrArgAsnLysGlyMetProGlnGlyLysGlySerTyrGlyArg-----GlnProHi	402
Db	2006	CGCAACGAGAGAGGTT-----GAAAGTCTCTCAAGAGCGCAAGACGAGGCTTC	2056
Qy	402	sSerAsnArgArg-----PheSerSerArgArg-----ArgAs	413
Db	2057	TCCATCAAGAGGCGAATACCTCGGCGAGCGGCTTCAAGAGAGAGAGATACATTTCGGA	2116

QY 413 pAspSerSerGluSerSerAspSerGlySerSerSerGlu----- 426
Db 2117 CGACGACTCCACGAGTCCCGACGAGAGGACACACGAGCTGCCAAGAGAGAGCAA 2176
QY 427 -----SerAspGlyAsp 430
Db 2177 GCCCCCATCCGACGCGCAT 2195

RESULT 4

US-08-258-442-10
; Sequence 10, Application US/08258442
; Patent No. 5670621
; GENERAL INFORMATION:
; APPLICANT: Donahue, Brian A.
; APPLICANT: Toney, Jeffrey H.
; APPLICANT: Bruhn, Suzanne L.
; APPLICANT: Pil, Pieter M.
; APPLICANT: Brown, Steven
; APPLICANT: Kellelt, Patti
; APPLICANT: Essigmann, John M.
; APPLICANT: Lippard, Stephen J.
; TITLE OF INVENTION: DNA Structure Specific Recognition
; TITLE OF INVENTION: Protein and Uses Therefor
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: 2 Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,442
FILING DATE:

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/539,906
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-4787AAA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2384 base pairs
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA

ORIGINAL SOURCE:
ORGANISM: Drosophila melanogaster
IMMEDIATE SOURCE:
CLONE: Drosophila SSRP - composite sequence
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 2
MAP POSITION: 60A 1-4

FEATURE:
NAME/KEY: CDS
LOCATION: 123...2291
US-08-258-442-10

Alignment Scores: 0.000459 Length: 2384
Pred. No.: 138.50 Matches:
Score:

Percent Similarity: 31.91% Conservative: 50
Best Local Similarity: 21.20% Mismatches: 136
Query Match: 6.08% Indels: 182
DB: 1 Gaps: 23

US-09-700-696C-2 (1-430) x US-08-258-442-10 (1-2384)

QY 16 GlyLeuArgMetSerIleTyrProLysSerThrGly-AsnLysGlyPheGluAspGlyAs 35
Db 1187 GGAGCGAGGATTCATCTATATCCCAAGCCACCCTGCATATCCGCTTTGAGGAG----- 1241
QY 35 pAspAlaIleSerLysLeuHisaspGlnGluGluTyrGlyAla----- 49
Db 1242 -----ATTAGTCTCTGTAACCTTTCGCCGAGCGCGGATCCACGCGATCTTTCGACTT 1294
QY 50 ---AlaLeuIleArgAsnMetGlnHisIleMetGlyProValThrAlaIleLysLe 68
Db 1295 CGAAGTCAGCTCAAGAACCGACTGTTTCATCTTCTCTCCATC----- 1340
QY 68 uLeuGlyGluGlnAsnLysGluAsnThrProArgAsnValLeuAsnIleleProAlaSe 88
Db 1341 -----GAGAAGGAGGAG----- 1352
QY 88 rMetAsnTyrAlaLysAlaHisSerLysAspLysLysLysProGlnArgAspSerGlnAl 108
Db 1353 -----TATGCCAAGCTC----- 1364
QY 108 aGlnLysSerProValLysSerLysSerThrHisArgIleGlnHisAsnIleAspTyrLe 128
Db 1365 -----TTCGACTACAT 1375
QY 128 uLys-----HisLeuSerLysValLysLysIleProSerAspPheGluGlySe 144
Db 1376 CACACAGAGAGAGTTGCATGTCCAGCAACATGGGCAAG-----GACAAGAG 1420
QY 144 rGlyTyrThrAspLeuGlnGlyArgGlyAspAsnAspIleSerProPheSerGlyAspGl 164
Db 1421 CGGCTACAGGACGTG---GACTTTGTGTGATTCCGAC-----AACGAGAA 1462
QY 164 yGlnProPheLysAspIleProGly---LysGlyGluAlaThrGlyProAspLeuGlu 183
Db 1463 CGAACCCAGATGCCCTATCTGCTCGCTCAAGGCTGAGCGAGGAGGAGGAGGAGAGA 1522
QY 183 yLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAspTh 203
Db 1523 CGACGAT-----GGCGACTCGGATGAAGAGTCCACGCGATGAGGACTT 1564
QY 203 rLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsnThrIleGl 223
Db 1565 C---AAGCCACAGAGAACGATCCGATGTGCCGAGGAGATGATGACAGCACGTGGAGAG 1621
QY 223 yThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGluGlySe 243
Db 1622 TGATTCGGACGAT-----GACAGCGATGCTAGTGGC-----GGCGG 1657
QY 243 rAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGlyAsnArgVa 263
Db 1658 AGCGCAGCAGCGCGCGGCCCAAGAAAAAGAGAGAGAGAGTCCGAGAGAGAGAGAAAA 1717
QY 263 lAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrProAlaPr 283
Db 1718 GGAGAAAAAACACAGGAG 1756
QY 283 oSerLysGluLysArgLysGluGlySer----- 292
Db 1757 CTCGAAG 1816
QY 293 ---SerAspAlaAlaGluSer-----ThrAsnTyrAsnGluI 304
Db 1817 GCTGAACGACACGCGCGAGAGAGATCAAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAG 1876
QY 304 eProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsnArgAsnGlnAl 324

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Db 1877 GCACAAGAGCGCGCGAGATGTGAAGAGCTGAAGACAAAGTCCAAAGTGGAGATGC 1936
Qy 324 aThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGlyLeuProIlePr 344
Db 1937 GCGCGCCAAAGACAAAGACGCGCTAC----- 1961
Qy 344 oSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsnGlyProSerHi 364
Db 1961 ----- 1961
Qy 364 sGluAsnIleIleThrHisGlyArgLysTyrHisTyrValProHisArgGlnAsnAsnSe 384
Db 1962 -----CACGACGAGATCGCAACTACAAAGCTGAAGCGGCGGTGACAG 2005
Qy 384 rThrArgAsnLysGlyMetProGlnGlyLysSerTrpGlyArg-----GlnProHi 402
Db 2006 CGACAACGAGAGGGT-----GGAAAGTCTCCAAAGAGCGCAAGACGAGCGCTTC 2056
Qy 402 sSerAsnArgArg-----PheSerSerArgArg-----ArgAs 413
Db 2057 TCCATCCAAGAGCGGAATACCTCGGCGAGCGGCTTCAAGACGAGGAGGTACATTTCGGA 2116
Qy 413 pAspSerSerGluSerAspSerGlySerSerSerGlu----- 426
Db 2117 CGACGACTCCACACGCTCCGACGACGAGACAGCAACAGCAGCTGCCAAGAAGAGAGCA 2176
Qy 427 -----SerAspGlyAsp 430
Db 2177 GCCCCCATTCGACGCGAT 2195

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RESULT 5

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US-08-328-809-5
; Sequence 5, Application US/08328809
; Patent No. 5705334
; GENERAL INFORMATION:
; APPLICANT: Lippard, Stephen J.
; APPLICANT: Essigmann, John M.
; APPLICANT: Donahue, Brian A.
; APPLICANT: Toney, Jeffrey H.
; APPLICANT: Bruhn, Suzanne L.
; APPLICANT: Fil, Pieter M.
; APPLICANT: Brown, Steven
; APPLICANT: Kelleff, Patti
; TITLE OF INVENTION: Uses For DNA Structure-Specific
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Administrator, Testa, Hurwitz & Thibault
; STREET: 53 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,809
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fenton, Gillian M.
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: MIT-023 (5473/24)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7000
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2384 base pairs
; TYPE: nucleic acid

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; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Drosophila melanogaster
; IMMEDIATE SOURCE:
; CLONE: Drosophila SSRP - composite sequence
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 2
; MAP POSITION: 60A 1-4
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 123...2291
US-08-328-809-5

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Alignment Scores:
Pred. No.: 0.000459 Length: 2384
Score: 138.50 Matches: 99
Percent Similarity: 31.91% Conservative: 50
Best Local Similarity: 21.20% Mismatches: 136
Query Match: 6.08% Indels: 182
DB: 1 Gaps: 23

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US-09-700-696C-2 (1-430) x US-08-328-809-5 (1-2384)
Qy 16 GlyLeuArgMetSerIleTyrProLysSerThrGly-AsnLysGlyPheGluAspGlyAs 35
Db 1187 GGAGCGAGGATTCATCTATATCCAAAGCCACCGCTGCATATCCGCTTTGAGGAG---- 1241
Qy 35 pAspAlaIleSerLysLeuHisaspGlnGluGluTyrGlyAla----- 49
Db 1242 -----ATTAGTTCTGTGAACTTTCCCGCAGCGCGGATCCACGCGATCTTTCGACTT 1294
Qy 50 ---AlaLeuIleArgAsnAsnMetGlnHisIleMetGlyProValThrAlaIleLysLe 68
Db 1295 CGAAGTCACGCTCAAGAACCGAAGTGTTCATCTTCTCTCCATC----- 1340
Qy 68 uLeuGlyGluAsnLysGluAsnThrProArgAsnValLeuAsnIleIleProAlase 88
Db 1341 -----GAGAAGGAGGAG----- 1352
Qy 88 rMetAsnTyrAlaLysAlaHisSerLysAspLysLysLysProGlnArgaspSerGlnAl 108
Db 1353 -----TATGCCAAGCTC----- 1364
Qy 108 aGlnLysSerProValLysSerLysSerThrHisArgIleGlnHisAsnIleAspTyrLe 128
Db 1365 -----TTCGACTACAT 1375
Qy 128 uLys-----HisLeuSerLysValLysLysIleProSerAspPheGluGlyse 144
Db 1376 CACACAGAGAGAGTTGCATGTCAGCAACATGGGCAAG-----GACAAGAG 1420
Qy 144 rGlyTyrThrAspLeuGlnIleuArgGlyAspAsnAspIleSerProPheSerGlyAspGI 164
Db 1421 CGGCTACAGACGCTG---GACTTTGGTGTATCCGAC-----AACGAGAA 1462
Qy 164 yGlnProPheLysAspIleProGly---LysGlyGluAlaThrGlyProAspLeuGluI 183
Db 1463 CGAACCCAGATGCTCTATCTGGCTCGCTCAAGCTGAGCGGAGGAGGAGGAGGACGA 1522
Qy 183 yLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAspTh 203
Db 1523 CGACGAT-----GGCGACTCGGATGAAGAGTCCACGATGAGGACTT 1564
Qy 203 rLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsnThrIleGI 223
Db 1565 C---AAGCCCAACGAGACGAGTCCGATGTGCCGAGGAGTATGACAGCAACGCTGGAGAG 1621
Qy 223 yThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGluGlyse 243
Db 1622 TGATTCCGACGAT-----GACAGCGATGCTAGTGGC-----GGCGG 1657

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1421 CGCTACAGACGTG--GACTTTGGTGTATCGGAC-----AACGAGAA 1462
164 yGlnProPheLysAspIleProGly---LysGlyGluAlaThrGlyProAspLeuGluGl 183
1463 CGAACACAGATGCTATCTGCTCGCTCAAGTGTAGCGGAGGAGGAGGAGGAGGAGGAG 1522
183 yLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAspTh 203
1523 CGACGAT-----GGCGACTCGGATGAGAGTCCACCGATGAGGACTT 1564
203 rLysLysProGlyTyrrAsnGluIleProGluArgGluGluAsnGlyGlyAsnThrIleGl 223
1565 C---AAGCCCAAGACGAGACGAGTCCGATGTGGCGGAGAGTATGACAGCAACATGGAGAG 1621
223 yThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGluGlySe 243
1622 TGATTCGACGAT-----GACACGATGCTAGTGGC-----GGCGG 1657
243 rAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGlyAsnArgVa 263
1658 AGCGACAGACGCGCGCGCCCAAGAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 1717
263 lAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrrProAlaPr 283
1718 GGAGAAAACACAG 1756
283 oSerLysGluLysArgLysGluGlySer----- 292
1757 CTCCAAG 1816
293 ---SerAspAlaAlaGluSer-----ThrAsnTyrrAsnGluI 304
1817 GCTGACGACAGACGCGCGGAGAGATCATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1876
304 eProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsnArgAsnGlnAl 324
1877 CGCCAAAGAGCGCGCGAGAGATGTGAAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 1936
324 aThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGlyLeuProIlePr 344
1937 GCGCGCCCAAG 1961
344 oSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsnGlyProSerHi 364
1961 ----- 1961
364 sGluAsnIleIleThrHisGlyArgLysTyrrHisTyrrValProHisArgGlnAsnAsnSe 384
1962 -----CACGACGAGATGCGCAACTTACAAAGCTTCAAGAGAGAGAGAGAGAGAGAG 2005
384 rThrArgAsnLysGlyMetProGlnGlyLysGlySerTyrGlyArg-----GlnProHi 402
2006 CGACAAACGAGAGGT-----GGAAAGTCTTCAAGAGAGAGAGAGAGAGAGAGAGAG 2056
402 sSerAsnArgArg-----PheSerSerArgArg-----ArgAs 413
2057 TCCATCAAG 2116
413 pAspSerSerGluSerSerAspSerGlySerSerGlySerSerGlySer----- 426
2117 CGAGACTTCCACAGCTCGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2176
427 -----SerAspGlyAsp 430
2177 GCCCCCATCCGACGCGGAT 2195

RESULT 7
PCT-US92-11107-10
; Sequence 10, Application PC/TUS9211107
; GENERAL INFORMATION:
; APPLICANT: Donahue, Brian A.
; APPLICANT: Toney, Jeffrey H.
; APPLICANT: Bruhn, Suzanne L.

APPLICANT: Pil, Pieter M.
APPLICANT: Brown, Steven
APPLICANT: Kelllett, Patti
APPLICANT: Essigmann, John M.
APPLICANT: Lippard, Stephen J.
TITLE OF INVENTION: DNA Structure Specific Recognition
TITLE OF INVENTION: Protein and Uses Therefor
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: 2 Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/11107
FILING DATE: 19921218
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/539,906
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-4787AAA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2384 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Drosophila melanogaster
CLONE: Drosophila SSRP - composite sequence
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 2
MAP POSITION: 60A 1-4
FEATURE:
NAME/KEY: CDS
LOCATION: 123..2291
PCT-US92-11107-10
Alignment Scores:
Pred. No.: 0.000459 Length: 2384
Score: 138.50 Matches: 99
Percent Similarity: 31.91% Conservative: 50
Best Local Similarity: 21.20% Mismatches: 136
Query Match: 6.08% Indels: 182
DB: 5 Gaps: 23
US-09-700-696C-2 (1-430) x PCT-US92-11107-10 (1-2384)
Qy 16 GlyLeuArgMetSerIleTyrrProLysSerThrGly-AsnLysGlyPheGluAspGlyAs 35
Db 1187 GGAGCGAGGATTCATCTATATCCACAGCCACGCGTCATATCCGCTTTGAGGAG---- 1241
Qy 35 pAspAlaIleSerLysLeuHisAspGlnGluThrGlyAla----- 49
Db 1242 -----ATTAGTCTGTGAACTTTGCCCGCGAGCGCGGATCCACGCGATTTTCGACTT 1294
Qy 50 ---AlaLeuIleArgAsnAsnMetGlnHisIleMetGlyProValThrAlaIleLysLe 68

Db 1295 CGAAGTGACGCTCAAGACGGAACGTGTTCACATCTTCTCCCTCCATC----- 1340
Qy 68 uLeuGlyGluGluAsnLysGluAsnThrProArgAsnValLeuAsnIlelleProAlaSe 88
Db 1341 -----GAGAAAGGAGGAG----- 1352
Qy 88 rMetAsnTyrAlaLysAlaHisSerLysAspLysLysProGlnArgAspSerGlnAl 108
Db 1353 -----TATGCCAAGCTC----- 1364
Qy 108 acLysSerProValLysSerLysSerThrHisArgIleGlnHisAsnIleAspTyrLe 128
Db 1365 -----TTCGACTACAT 1375
Qy 128 uLys-----HisLeuSerLysValLysLysLysProSerAspPheGluGlySe 144
Db 1376 CACACAGAAGAGTTCATGTGCACACATCGGCAAG-----GACACAGAG 1420
Qy 144 rGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGl 164
Db 1421 CGGCTACAAAGACGTG--GACTTGTGATTCGGAC-----AACGAGAA 1462
Qy 164 yGlnProPheLysAspIleProGly--LysGlyGluAlaThrGlyProAspLeuGluGl 183
Db 1463 CGAACCAAGTCTATCGCTCGCTCAAGCTCGAGCGGAGGAAAGAGGAGGACGA 1522
Qy 183 yLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAspTh 203
Db 1523 CGACCAT-----GGCGACTCGGATGAGAGTCCACGGATGAGGACTT 1564
Qy 203 rLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsnThrIleGl 223
Db 1565 C--AAGCCCAACAGAGACGATCGATGTGGCCGAGGAGTATGACACACCGTGGAGAG 1621
Qy 223 yThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGluGlySe 243
Db 1622 TGATTCGGACGAT-----GACAGCGATGCTAGTGC-----GGCGG 1657
Qy 243 rAsnAspIleMetGlySerThrAsnPhelGlyLeuProGlyArgGluGlyAsnArgVa 263
Db 1658 AGCGCAGCAGCGCGCGCGCAAGAAAGAGAGAGAGTCCGAGAGAAAGAGAA 1717
Qy 263 lAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrProProAlaPr 283
Db 1718 GGAGAAACACACAGGAGAGAGAGACAAAG-----AAACC 1756
Qy 283 oSerLysGluLysArgLysGluGlySer----- 292
Db 1757 CTCACAGAGAGAGAGGACTCTGCGCAACCCACAGCGCCACCGCTTTCATGCTCTG 1816
Qy 293 -----SerAspAlaIleGluSer-----ThrAsnTyrAsnGluIle 304
Db 1817 GGTGAACGACACGCGCGAGAGCATCAAGAGGGAATCCGGGCATAAAGGTTACCGAGAT 1876
Qy 304 eProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsnArgAsnGlnAl 324
Db 1877 GCCCAAGAGGCGCGGAGATGTGAGGAGCTGAAGGACACAGTCCAAAGTGGAGATGC 1936
Qy 324 aThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGlyLeuProIlePr 344
Db 1937 GCGCGCCCAAGGACACAGCGCTAC----- 1961
Qy 344 oSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsnGlyProSerHi 364
Db 1961 ----- 1961
Qy 364 sGluAsnIlelleThrHisGlyArgLysTyrHisTyrValProHisArgGlnAsnAsnSe 384
Db 1962 -----CACGACGAGATGCGCACTACAGCTCAAGCGCGCGGTGACAG 2005
Qy 384 rThrArgAsnLysGlyMetProGluGlyGlySerTyrGlyArg-----GlnProHi 402
Db 2006 CGACACAGAGAGGGT-----GAAAGTCTCCAGAGCGCAGACGAGGCTTC 2056

Qy 402 sSerAsnArgArg-----PheSerSerArgArg-----ArgAs 413
Db 2057 TCCATCCAAAGAGCGCAATACCTCGGGCAGCGCTTCAAGAGCAAGAGTACATTTCCGA 2116
Qy 413 pAspSerSerGluSerSerAspSerGlySerSerGlu----- 426
Db 2117 CGAGACTCCACGACTCGGACGACGAGAGGACACGAGCTGCCAAGAGAGACAA 2176
Qy 427 -----SerAspGlyAsp 430
Db 2177 GCCCCCATCGACGCGCAT 2195
RESULT 8
US-08-320-559-27
Sequence 27, Application US/08320559
Patent No. 5633135
GENERAL INFORMATION:
APPLICANT: Croce, Carlo
APPLICANT: Canaan, Eli
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods for
Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the
TITLE OF INVENTION: All-1 Region
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5633135ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/320,559
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/062,443
FILING DATE: 14 MAY 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/971,094
FILING DATE: 30-OCT-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,830
FILING DATE: 27-MAY-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/805,093
FILING DATE: 11-DEC-91
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0855
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 9370 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 469..4032
US-08-320-559-27
Alignment Scores:

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Pred. No.: 0.00499 Length: 9370
Score: 137.00 Matches: 100
Percent Similarity: 34.70% Conservative: 61
Best Local Similarity: 21.55% Mismatches: 192
Query Match: 6.01% Indels: 113
DB: 1 Gaps: 17

US-09-700-696C-2 (1-430) x US-08-320-559-27 (1-9370)

QY 37 AlaIleSerLysLeuHisAspGlnGluTyrGlyAlaAlaLeuIleArgAsnMet 56
DB 1938 GCAGCTGACAACTGGCTGACCAAGTCCAGCAGCGCGCCGACAGGAGGCGCCAG 1997
QY 57 GlnHisIleMetGlyProValThrAlaIleLysLeuGluGluAsnLysGluAsn 76
DB 1998 GAGCAC---AGAGCCCCCAGCGCGCCAGAGAGTAGGAGCAGCAGCAGTGCCAC 2054
QY 77 ThrProArgAsnValLeuAsn-----IleIleProAlaSerMetAsnTyrAlaLysAla 94
DB 2055 GAGTC-AGGACATTCGTAATCCAAAGATCTCTCCC-----CTAAAGCT 2098
QY 95 HisSerLysAspLysLysLysProGlnArg-----AspSerGlnAlaGln 109
DB 2099 CC-AGCAAGCCCCCGCGGCCCCAGCCGAGCCGCCAGCCGCGGAAAGAGGAGCTGTCCAG 2157
QY 110 LysSerProValLysSerLysSerThrHisArgIleGlnHisAsnIleAspTyrLeuLys 129
DB 2158 AAGTCTCGGCACAGCAGGAGCCCCCAAGAGGAAACCTGTGGACCAACCAACCCCAA 2217
QY 130 HisLeuSerLysValLysLysIleProSerAspPheGluGlySerGlyTyrThrAspLeu 149
DB 2218 -----AAACCTGTCAAGGCTCTGCCCGGCGAGGTTCCAGCAGCCGCTG 2262
QY 150 GlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGlyGlnProPheLysAsp 169
DB 2263 CAGGGGGAAGGAGGACAGCGGCTCTCTCCCTATGGCTCCCGAGACAGACTTCCAAAGAC 2322
QY 170 IlePro-----GlyLysGlyGlu----- 175
DB 2323 AAGCCCAAGGTGAAGACGAAGAGCGCGCCCGCGCCAGCAGCAAGCAACCAAGCCCA 2382
QY 176 AlaThrGlyProAspLeuGlyLysAspIleGlnThrGlyPheAlaGlyProSerGlu 195
DB 2383 GCAGTGGCCCCCTCCAGTGAGAAGAAGACACAGAGCTCCCTCCCTGCCCCCTCTAAG 2442
QY 196 AlaGluSer-----ThrHisLeuAspThrLysLysProGlyTyr--- 208
DB 2443 GCTCTCTCAGCCCGCAGAACCGCGAAGACAAATGTGGAGACAGGACCCCTGACACTTT 2502
QY 209 -----AsnGluIleProGluArgGluGluAsnGlyGlyAsnThr 221
DB 2503 GCTCTTGTCTCCCTGACTGAGAGCGCGCGCCCGCCAGCAGTGGCGGCGCAGCAGACT 2562
QY 222 IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGlu 241
DB 2563 AGTGGTGGCGCCCAAGCGGTGGTGGTCCAGGAGACAGCGCGCAAGAGCAGACTCCCATTTG 2622
QY 242 GlySerAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGlyAsn 261
DB 2623 CCTTTGAGACACCAAGCTGCTCTCACCGCTCAGGAGCAGCTCTCCCGCAAGAGCTTG 2682
QY 262 ArgVal-----AspAlaGlySerGlnAsnAla 270
DB 2683 ATGGTGAAGATCACCCCTAGACCTGCTCTCTCGGATACCCAGCCTCCCGGAGGGGAGC 2742
QY 271 HisGlnGlyLysValGluPheHisTyrProProAlaProSerLysGluLysArgLysGlu 290
DB 2743 CGCCAGAGGAAGACGAAGAATAACAGCCCGCGCAGGAGGAAGACAGCTCTGTGAAG 2802
QY 291 GlySerSerAspAlaAlaGluSerThrAsnTyrAsnGluIleProLysAsnGlyLysGly 310
DB 2803 AGGAGCTCAGACACTCA-----AGCAAGTTGGCCAAAGAGAGAGGGT 2847
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QY 311 SerThrArgLysGlyValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGluLysGln 330
DB 2848 GAAGCAGAAAGAGACTGTGAT-----AACAAAGAAATC 2880
QY 331 ArgPheProSerLysGlyLysSerGlnGlyLeuProIleProSerArgGlyLeuAspAsn 350
DB 2881 AGA-----CTGAGAG 2892
QY 351 GluIleLysAsnGluMetAspSerPheAsnGlyProSerHisGluAsnIleIleThr--- 369
DB 2893 GAAATCAATCACAGTCACTTCTTCATCTCTCCCAAGAAATCTTCTTAAACAAAG 2952
QY 370 -----HisGlyArgLysTyrHisTyrValProHisArgGlnAsn 382
DB 2953 CCCTCCAGCCCTCTCTCACAGTCTCTCAAGAGGAAATGCTCCCGCCCGCCCGTCTCC 3012
QY 383 AsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySer----- 396
DB 3013 TCGTCTCTCCAGAGCCAGCCAGCCTTCAAGGCTTCAAGGCTCAAGCGGGAAGCAGACACC 3072
QY 397 TrpGlyArgGlnPro-----HisSerAsnArgArgPheSerSer 409
DB 3073 TGTGGCAGGAGCCCTCCCAAGGTGCCAGCAGTACCAGAGCAACCAACAGACTCTTCC 3132
QY 410 ArgArgArgAspAspSerSerGluSerSerAspSerGlySerSerSerGlu----- 426
DB 3133 ATTCCCAAGCAGAGAGTAGAGGGGAAGGGCTCCAGAGGCTCTCGGAGCACAAGGGT 3192
QY 427 SerAspGlyAsp 430
DB 3193 TCTTCCGAGAT 3204

RESULT 9
US-08-545-860D-27
; Sequence 27, Application US/08545860D
; Patent No. 6040140
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Canaan, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
; TITLE OF INVENTION: For Detection and Treatment of Acute Leukemias
; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1 Region
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
; ADDRESSEE: No. 6040140 is
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,860D
; FILING DATE: 07-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04496
; FILING DATE: 22-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10930
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/327,392
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/320,559
; FILING DATE: 11-OCT-1994
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 08/062,443
; FILING DATE: 14-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/971,094
; FILING DATE: 30-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/888,839
; FILING DATE: 27-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/805,093
; FILING DATE: 11-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca Esq., Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1262
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9370 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 469..4032
US-08-545-860D-27

Alignment Scores:
Pred. No.: 0.00499 Length: 9370
Score: 137.00 Matches: 100
Percent Similarity: 34.70% Conservative: 61
Best Local Similarity: 21.55% Mismatches: 192
Query Match: 6.01% Indels: 113
Dbs: 3 Gaps: 17

US-09-700-696C-2 (1-430) x US-08-545-860D-27 (1-9370)
QY 37 AlaIleSerLysLeuHisAspGlnGluGluTyrGlyAlaAlaLeuIleArgAsnMet 56
Db 1938 GCAGCTGGACAACTGGCTGACCAAAAGTCAGCCAGCCAGCTGCCGCCACAGAGGGCCCCAG 1997
QY 57 GlnHisIleMetGlyProValThrAlaIleLysLeuGluGluGluAsnLysGluAsn 76
Db 1998 GAGCAC---AGAGCCCCACCGCGGCACCCAGAGAGTAAAGGCAGCAGCAGTGCAC 2054
QY 77 ThrProArgAsnValLeuAsn-----IleIleProAlaSerMetAsnTyrAlaLysAla 94
Db 2055 GAGTC-AGGAGCATTTCTGAATCAAAAGATCTCTCCCT-----CTAAAGGCT 2098
QY 95 HisSerLysAspLysLysLysProGlnArg-----AspSerGlnAlaGln 109
Db 2099 CC-AGCAAGCCCCCGCGGCCCCACCCGAAAGCCCCCAGGAGGAGGAGTCTCAG 2157
QY 110 LysSerProValLysSerLysSerThrHisArgIleGlnHisAsnIleAspTyrLys 129
Db 2158 AAGTCTCCGGCACAGCAGGAGGCCCCCACAAGAGGCAAAACCGTTTGGAAACCAACCCCAA 2217
QY 130 HisLeuSerLysValLysLysIleProSerAspPheGluGlySerGlyTyrThrAspLeu 149
Db 2218 -----AAACCTGTCAAGGCTCTGCCCGGCGAGGTTTCAGGACCGCCG 2262
QY 150 GlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGlnProPheLysAsp 169
Db 2263 CAGGGGGAAGGAGGAGCAGGGCTCTCTCTATGGCTCCCGAGACCAGACTTCCAAAGAC 2322
QY 170 IlePro-----GlyLysGlyGlu----- 175
Db 2323 AAGCCCCAAGTGAAGACGAAGAGGAGCGGCCCGCGCGCAGCAAGCAACGAACCAAGCCA 2382
QY 176 AlaThrGlyProAspLeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGlu 195

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Db 2383 GCAGTGCCCCCTCCAGTGAGAAGAAGCAAGAGCTCCCTCCTGCCCCCTCTAAG 2442
QY 196 AlaGluSer-----ThrHisLeuAspThrLysLysProGlyTyr--- 208
Db 2443 GCTCTCTCAGGCCAGAACCCGGAAGGACAATGTGAGGACAGGACCCCTTGACACTTT 2502
QY 209 -----AsnGluIleProGluArgGluGluAsnGlyGlyAsnThr 221
Db 2503 GCTCTTTTCCCTGACTGAGAGCCAGGCCCCACCCACAGTGCGCAGCGCAGCAGACT 2562
QY 222 IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGlu 241
Db 2563 AGTGGCTGCCCAAGCCGTGTGTGTCAGGAGGACAGCGCGCAAGACAGACTCCCATTTG 2622
QY 242 GlySerAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGlyAsn 261
Db 2623 CTTTTCAGAGACACCAAGCTGCTCTCACCGCTCAGGGACACTCTCTCCCCACCAAGCTTG 2682
QY 262 ArgVal-----AspAlaGlySerGlnAsnAla 270
Db 2683 ATGCTGAAGATCACCTAGACCTGTCTCTCGGATACCCAGCCTCCCGGAGGGGAGC 2742
QY 271 HisGlnGlyLysValGluPheHisTyrProProAlaProSerLysGluLysArgLysGlu 290
Db 2743 CCCCAGAGAAAGCAGAAAGATAAACAGCCCGCCGAGGGAAGAACAGCAGCTCTGAGAAG 2802
QY 291 GlySerSerAspAlaAlaGluSerThrAsnTyrAsnGluIleProLysAsnGlyLysGly 310
Db 2803 AGGAGCTCAGACAGCTCA-----AGCAAGTTGGCCCAAAAGAGAGAGGCT 2847
QY 311 SerThrArgLysGlyValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGluLysGln 330
Db 2848 GAAGCAGAAAGAGAGACTGTGAT-----AACAGAAATCTCTATAAACAAAG 2880
QY 331 ArgPheProSerLysGlyLysSerGlnGlyLeuProIleProSerArgGlyLeuAspAsn 350
Db 2881 AGA-----CTGGAGAAG 2892
QY 351 GluIleLysAsnGluMetAspSerPheAsnGlyProSerHisGluAsnIleIleThr--- 369
Db 2893 GAATCAATCACAGTCATCTTCACTTCTCCTCCACAAAGATCTCTATAAACAAAG 2952
QY 370 -----HisGlyArgLysTyrHisTyrValProHisArgGlnAsn 382
Db 2953 CCCTCAGGCCCTCTCTCACAGTCTCTCAAGAGAAATGCTCCCGCCGACCCGCTGCC 3012
QY 383 AsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySer----- 396
Db 3013 TGTCTCTCCAGAGCCAGCCAGCCTTGACCTTAAGAGGTCAAGCGGGAAGCAGACACC 3072
QY 397 TrpGlyArgGlnPro-----HisSerAsnArgArgPheSerSer 409
Db 3073 TGTGCCAGGACCTCCCAAAAGTGCACAGTACCAGAGCAACCAAGACTCTTCC 3132
QY 410 ArgArgArgAspAspSerSerGluSerSerAspSerGlySerSerSerGlu----- 426
Db 3133 ATTCCCAAGCAGAGAAGTAGAGGGAAGGCTCCAGAAGCTCTCTCGGAGCACAAGGCT 3192
QY 427 SerAspGlyAsp 430
Db 3193 TCTTCGGAGAT 3204

RESULT 10
PCT-US94-04496-27
; Sequence 27, Application PC/TUS9404496
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Canaani, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
; TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1
; NUMBER OF SEQUENCES: 86

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Db 2644 CTTTTCAGACACCAAGCTGCTCTACCCGCTCAGGAGACTCTCTCCCCACAAAGCTTG 2703
QY 262 ArgVal-----AspAlaGlySerGlnAsnAla 270
Db 2704 ATGCTGAAGATCACTCCCTAGACCTGCTCTCTCGGATACCCAGCTCTCCCGGAAGGGAGC 2763
QY 271 HisGlnGlyValGluPheHisTyrProProAlaProSerLysGluLysArgLysGlu 290
Db 2764 CGCAGAGGAAGACAGAGATAAAGCCCGCCGAGGGAAGACACAGCTCTCGAGAAG 2823
QY 291 GlySerSerAspAlaAlaGluSerThrAsnTyrAsnGluLeuProLysAsnGlyLysGly 310
Db 2824 AGGAGCTCAGACACTCA-----AGCAAGTTGCCCAAAAAGAGAGAGGT 2868
QY 311 SerThrArgLysGlyValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGluLysGln 330
Db 2869 GAAGCAGAAAGAGACTGTGAT-----AACAAAGAAATC 2901
QY 331 ArgPheProSerLysGlyLysSerGlnGlyLeuProfileProSerArgGlyLeuAspAsn 350
Db 2902 AGA-----CTGGAGAAG 2913
QY 351 GluIleLysAsnGluMetAspSerPheAsnGlyProSerHisGluAsnIleIleThr--- 369
Db 2914 GAAATCAATCAGCTCATCTTCATCTTCATCTCCACAAAGATCTTCTAAACAAAG 2973
QY 370 -----HisGlyArgLysTyrHisTyrValProHisArgGlnAsn 382
Db 2974 CCTCCAGGCCCTCTCACAGTCTCTCAAGAGAGAAATGCTCCCGCCGACCCGCTGTC 3033
QY 383 AsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySer----- 396
Db 3034 TCGTCTCTCCAGAGCCAGCAGCTGCACTTAAGAGGTCAAAGCGGGAAGCAGACACC 3093
QY 397 TrpGlyArgGlnPro-----HisSerAsnArgArgPheSerSer 409
Db 3094 TGTGGCCAGGACCTCCCAAAAGTGCAGCAGTACCAAGAGCAACACCAAGACTCTTCC 3153
QY 410 ArgArgArgAspSerSerGluSerSerAspSerGlySerSerSerGlu----- 426
Db 3154 ATTCCCAACAGAGAGAGTAGAGGGGAGGGTCCAGAAAGTCTCTCGAGCACAAGGT 3213
QY 427 SerAspGlyAsp 430
Db 3214 TCTTCGGAGAT 3225

RESULT 13
PCT-US94-04496-25
Sequence 25, Application PC/TUS9404496
GENERAL INFORMATION:
APPLICANT: Croce, Carlo
APPLICANT: Canadani, Eli
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the ALL-1
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock, Washburn, Kurtz, Mackiewicz &
ADDRESSER: Norris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04496
FILING DATE:
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: DeLuca Esq., Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 9391 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 421...4053
PCT-US94-04496-25
Alignment Scores:
Pred. No.: 0.00501 Length: 9391
Score: 137.00 Matches: 100
Percent Similarity: 34.70% Conservative: 61
Best Local Similarity: 21.55% Mismatches: 192
Query Match: 6.01% Indels: 113
DB: 5 Gaps: 17

US-09-700-696C-2 (1-430) x PCT-US94-04496-25 (1-9391)

QY 37 AlaIleSerLysLeuHisAspGlnGluTyrGlyAlaAlaLeuIleArgAsnMet 56
Db 1959 GCAGCTGGAGCACTGGCTGACCAAGTCAGCCAGCCAGCTGCCACACGAGGGCCCCAG 2018
QY 57 GlnHisIleMetGlyProValThrAlaIleLysLeuLeuGluGluAsnLysGluAsn 76
Db 2019 GAGCAC---AGAGCCCCCAGCGGCAGCCAGAGAGTAAGGGCAGCAGCAGTCGCAC 2075
QY 77 ThrProArgAsnValLeuAsn-----IleIleProAlaSerMetAsnTyrAlaLysAla 94
Db 2076 GAGTC-AGGAGCATCTTGAATCAAGATCTCTCCCC-----CTAAGAAGCT 2119
QY 95 HisSerLysAspLysLysLysProGlnArg-----AspSerGlnAlaGln 109
Db 2120 CC-AGCAAGCCCCCGGGCCACCCGAAAGCCCCACCCGAGAGAGAGAGCTGTCAG 2178
QY 110 LysSerProValLysSerLysSerThrHisArgIleGlnHisAsnIleAspTyrLeuLys 129
Db 2179 AAGTCTCCGGCAGCAGCAGGAGCCGCCCAAAAGGCAAAACCGTTGGAAACCAACACCCAAA 2238
QY 130 HisLeuSerLysValLysLysIleProSerAspPheGluGlySerGlyTyrThrAspLeu 149
Db 2239 -----AACTCTCAAGGCTCTGCCCGGCAGGTTTCACGACACGCTG 2283
QY 150 GlnGluArgGlyAspAsnAspLysSerProPheSerGlyAspGlyGlnProPheLysAsp 169
Db 2284 CAGGGGGAAGGAGCCAGGGCTTCTTCCTATGGCTCCCGAGACCCAGACTTCCAAAGAC 2343
QY 170 IlePro-----GlyLysGlyGlu----- 175
Db 2344 AAGCCCAAGGTGAAGACGAAAGGAGCGGCCCGCGCAGCAAGCAACGAAACCCAGCCCA 2403
QY 176 AlaThrGlyProAspLeuGluLysAspIleGlnThrGlyPheAlaGlyProSerGlu 195
Db 2404 GCAGTGCCCCCTCCAGTGAGAGAGAGACACAGAGCTCCCTCCCTGCCCTCTTAAG 2463
QY 196 AlaGluSer-----ThrHisLeuAspThrLysLysProGlyTyr--- 208
Db 2464 GCTCTCAGGCCCCAGAACCCCGAAGGAGCAATAGTGGAGACAGGACCCCTCAGCATT 2523
QY 209 -----AsnGluIleProGluArgGluGluAsnGlyGlyAsnThr 221
Db 2524 GCTCTGTTCCTGACTGAGAGCCAGGGCCCAACCCCAAGTCAGTGGCAGCGCAGGACT 2583

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QY 222 IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValSerLeuValGlu 241
Db 2584 AGTGGCTGCCCAAGCCGCTGGTCCAGGAGCAGCGCAAGACACATCCCATG 2643
QY 242 GlySerAsnAspIleMetGlySerThrAsnPhelLysGluLeuProGlyArgGluGlyAsn 261
Db 2644 CCITTAGAGACACCAAGCTGCTCTCACCGCTCAGGACACTCTCCCCCAAGAGTTG 2703
QY 262 ArgVal 270
Db 2704 ATGCTGAAGATCATCCCTAGACCTGCTCTCTCGGATACCCAGCCTCCCGGAAGGGGAGC 2763
QY 271 HisGlnGlyLysValGluPheHisTyrProProAlaProSerLysGluLysArgLysGlu 290
Db 2764 CGCAGAGGAAGCAGGAAGATAAACACGCCGCCCGGAGGAGACACACTCTGGAAG 2823
QY 291 GlySerSerAspAlaAlaGluSerThrAsnTyrAsnGluIleProLysAsnGlyLysGly 310
Db 2824 AGGAGCTCAGACGCTCA-----AGCAAGTTGGCCAAAGAGAGAGGGT 2868
QY 311 SerThrArgLysGlyValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGluLysGln 330
Db 2869 GAAGCAGAAAGAGACTGTGAT-----AACAGAAATC 2901
QY 331 ArgPheProSerLysGlyLysSerGlnGlyLeuProIleProSerArgGlyLeuAspAsn 350
Db 2902 AGA-----CTGGAGAG 2913
QY 351 GluIleLysAsnGluMetAspSerPheAsnGlyProSerHisGluAsnIleThr--- 369
Db 2914 GAAATCAATACAGTCATCTTCATCTTCCTCCACAAAGAAATCTTCAAAACAAG 2973
QY 370 -----HisGlyArgLysTyrHisTyrValProHisArgGlnAsn 382
Db 2974 CCTCCAGGCCCTCTCACAGTCTCTAAAGAGGAAATGCTCCCGCCGCCACCGGTCC 3033
QY 383 AsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySer----- 396
Db 3034 TCGTCTCTCCAGAGCAGCAGCAAGCTGCACTTAAGAGGTCAAGCGGGAAGCAGACACC 3093
QY 397 TrpGlyArgGlnPro-----HisSerAsnArgArgPheSerSer 409
Db 3094 TGTGGCCAGGACCTCCCAAAAGTGCCAGCAGTACCAAGAGCAACACAAAGACTCTTCC 3153
QY 410 ArgArgArgAspAspSerSerGluSerSerArgSerSerGlySerSerGlu----- 426
Db 3154 ATCCCAACAGAGAGAGTAGAGGAGGAGGCTCCAGAGGCTCTCCGAGCACAAGGGT 3213
QY 427 SerAspGlyAsp 430
Db 3214 TCTTCGGAGAT 3225
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RESULT 14
US-08-568-459A-1
; Sequence 1, Application US/08568459A
; Patent No. 5849306
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/568,459A
; APPLICATION NUMBER: 07-DEC-1995
; FILING DATE: 07-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH21.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4084 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium vivax
; US-08-568-459A-1
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Alignment Scores:
Pred. No.: 0.00256 Length: 4084
Score: 134.50 Matches: 97
Percent Similarity: 36.42% Conservative: 80
Best Local Similarity: 19.96% Mismatches: 220
Query Match: 5.90% Indels: 89
DB: 2 Gaps: 21
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US-09-700-696C-2 (1-430) x US-08-568-459A-1 (1-4084)

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QY 2 AsnLysGluTyrSerLysSerAsnLysGluAsnThrHisAsnGlyLeuArgMetSerIle 21
Db 1724 AATAAATTCATAAGTGTAAACGCGAGGCTTTCAGACGCGCAGGTATCGTAACCTCT 1783
QY 22 TyrProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerLysLeu 41
Db 1784 TAT-----GATATCTAAACACAG--- 1801
QY 42 HisAspGlnGluGlyTyrGlyAlaAlaLeuIleArgAsnAsnMetGlnHisIleMetGly 61
Db 1802 ---GAGTTAGATGAATTTAACGAGGTGGCTTTTGAGAAATTAACAAACGCTGATGGT 1858
QY 62 ProValThrAlaIleLysLeuGly---GluGluAsnLysGluAsnThrProArgAsn 80
Db 1859 GCATATATTGAGTTATGCTGTTTGTTCGTTGAAGAGGCTTAAACAAATTAACCTCAGGAAGTT 1918
QY 81 ValLeuAsnIleIleProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLys 100
Db 1919 GTGACAAATGTGGCAATGCTCTAAATCTCAGGCC---ACCAATTCAAATCCGATAAGT 1975
QY 101 LysProGlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArg 120
Db 1976 CAGCTGTAGATAGTAGTAAGCGGAGAGGTCTCCA-----GGAGATCTACGCAT--- 2026
QY 121 IleGlnHisAsnIleAspTyrLeuLysHisLeuSerLysVal---LysLysIleProSer 139
Db 2027 -----GGAAATGTTTAAACAGTGGCCCAAGATAGTTCTACCACAGGTAAAGCTGTACGGGG 2080
QY 140 AspPheGluGlySerGlyTyrThrAspLeuGln-----GluArgLysAspAsnAsp 156
Db 2081 GATGTCGAAATGGAAATCAGACACCTGCAGAAACCGATGTACAGCGAGTATATTGCC 2140
QY 157 IleSerProPheSerGlyAspGlyGlnProPheLysAspIleProGlyLysGlyGlu--- 175
Db 2141 GAAAGTGTAAAGTGTAAAGATGTTGATCCGCAAGAAATCTGTAAAGTAAAGAGAGTACCGAC 2200
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QY 176 -----AlaThrGlyProAspLeuGluGlyLysAspIleGlnThrGlyPheAlaGly 192
Db 2201 ACTGCAAGCGTTACAGGATATGCGAAGCTGGAAAGGAA---AACTTAGCGCATCAAT 2257
QY 193 ProSerGluAlaGluSerThrHisLeuAspThrLysLysProGly----- 207
Db 2258 AGTCGACCTTCAGTCCACC-----GTTGAAGCAAAATAGCCCGAGGTGATGATCATGTGGAAC 2314
QY 208 -----TyrAsnGluIle 211
Db 2315 AGTCGATCTATACCTAGTAGAGTGGTGAAGAACCCCATTTGGTACCCCTATATATGTTG 2374
QY 212 ProGluArgGluAsnGlyGlyAsn-----Thr 221
Db 2375 AGGCATTCGAAGACAATAGTAGTCATGATGCGGAAATCAATGGCGAATCTCTGAT 2434
QY 222 IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGlu 241
Db 2435 TCAATAGTAGTAAGGTGAGACGGGAAGGGCAAGATAATGATGCGAAGGCTACTAA 2494
QY 242 GlySerAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGlyAsn 261
Db 2495 GATAGTAGTAATAGTTTCAGATGCTACGAGC-----TCTGCTACGGGTGAT 2539
QY 262 ArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrProPro 281
Db 2540 ACTACTGATGCGATTTGATAGGGAATTAATAAGGTGTTCTGAGGATAGGGATAAACT 2599
QY 282 AlaProSerLysGlyLysArgLysGlyGlySerSer-----AspAlaAlaGluSer 298
Db 2600 GTAGGAAGTAAGATGAGCGGGGGAAGATACTCTGCAAAATAGATGCGAGCATCTA 2659
QY 299 ThrAsnTyrAsnGluIleProLysAsnGlyLysGlySerThr-----ArgLysGly 315
Db 2660 GTTGTGTAGGATAGATTTCTGAGACAGCGCTGCTGAGCACTAATGATAGATCAAAA 2719
QY 316 ValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGluLysGlnArg-----PhePro 333
Db 2720 AATGACACGGAAGAACCGGGCGCTCTACCCCTGACAGTAAACAAAGTGAGGATGCAACT 2779
QY 334 SerLysGlyLysSerGlnGlyLeuProIleProSerArgGly-----LeuAspAsnGlu 351
Db 2780 GCGCTAAGTAACCCGAAGTTTAGATCAACAGAAAGTGGAGATAGAACTACTATGAT 2839
QY 352 IleLysAsnGluMetAspSerPheAsnGlyProSerHisGluAsnIleIleThrHisGly 371
Db 2840 ACAACTAACACAGTTTAGAAAAATAAATGAGGAAAGAAAGGATTTACAAAAGCATGAT 2899
QY 372 ArgLysTyrHisTyrValProHisArgGlnAsnAsnSerThrArg----- 386
Db 2900 TTTAAAGTAGATACGCGGATGAAGAACCAAAATTTCTGATCAAACTACAGATGACGAA 2959
QY 387 -----AsnLysGlyMetProGlnGlyLysGlySerTyrGlyArgGlnProHisSer 403
Db 2960 GGACATGACAGGATAGCATCAAAATGATAAGCAGAA-----AGGAGAAGCATATG 3013
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QY 423 SerSerSerGluSerAsp 428
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RESULT 15

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US-08-487-826B-1
; Sequence 1, Application US/08487826B
; Patent No. 5933827
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
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; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellemis, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbie Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4084 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium vivax
; US-08-487-826B-1

Alignment Scores:
Pred. No.: 0.00256 Length: 4084
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Best Local Similarity: 19.96% Mismatches: 220
Query Match: 5.90% Indels: 89
DB: 2 Gaps: 21
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US-09-700-696C-2 (1-430) x US-08-487-826B-1 (1-4084)

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QY 2 AsnLysGluTyrSerIleSerAsnLysGluAsnThrHisAsnGlyLeuArgMetSerIle 21
Db 1724 AATAATTCATAGTGTAAACCCAGAAAGGTTTCAGACGCGAGGTATCGTAATCTCT 1783
QY 22 TyrProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerLysLeu 41
Db 1784 TAT-----GATATACTAAACAG--- 1801
QY 42 HisAspGlnGluGlyTyrGlyAlaAlaLeuIleArgAsnAsnMetGlnHisIleMetGly 61
Db 1802 ---GAGTTAGATGAATTTAACGAGGTGGCTTTTGAAGATGAAATTAACAAACGCTGATGCT 1858
QY 62 ProValThrAlaIleLysLeuLeuGly---GluGluAsnLysGluAsnThrProArgAsn 80
Db 1859 GCATATATTGATGATGCTTTGTTCCGTTGAAGAGGCTAAATAAATACTCAGAAAGTT 1918
QY 81 ValLeuAsnIleIleProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLys 100
Db 1919 GTGACAAATGTGGCAATGCTGCTAAATCTCAGGCC---ACCAATTCAATCCGATAAGT 1975
QY 101 LysProGlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArg 120
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Db 2027 -----GGAAATGTTAAACAGTGGCGGCAAGATAGTTCTACACACAGGTAAAGCTGTACGGGG 2080
Qy 140 AspPheGluGlySerGlyTyrThrAspLeuGln-----GluAtgGlyAspAsnAsp 156
Db 2081 GATGGTCAAAATGGAATCAGACACCTGCAGAAAGCGATGTACAGCGAGTGAATATTGCC 2140
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Db 2201 ACTCAAGCGTTACAGGTATTGCCGAAGCTGGAAGGAA---AACTTAGCGCATCAAT 2257
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Db 2840 ACAACTAACAGTTTAGAAAATAAAATGGAGGAAAGAAAGGATTTACAAAAGCATGAT 2899
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Job time : 115 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

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Run on: November 30, 2003, 00:14:26 ; Search time 423 Seconds
(without alignments)
3349.212 Million cell updates/sec

Title: US-09-700-696C-2

Perfect score: 2279

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2190069 seqs, 1647345023 residues

Total number of hits satisfying chosen parameters: 4380138

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications NA -QEMT=fastCap -SUFFIX=rnpb -MINMATCH=0.1
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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-MAXLEN=200000000 -USRF=US09700696 @CGN_1_1_221 @runat_26112003_152634_14705
-NCFU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCKS=100
-LONGLOG -DEV TIMEOUT=30 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

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2: /cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq:
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17: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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Alignment Scores: 2.22e-213 Length: 1575
Pred. No.: 2.22e-213

2	2276	99.9	1662	12	US-10-311-840-3	Sequence 3, Appli
3	2276	99.9	1876	12	US-09-794-422-33	Sequence 33, Appl
4	2276	99.9	1969	12	US-09-794-422-45	Sequence 45, Appl
5	2276	99.9	2019	12	US-09-794-422-5	Sequence 5, Appli
6	2276	99.9	2112	12	US-09-794-422-7	Sequence 7, Appli
7	983.5	43.2	1682	12	US-09-794-422-3	Sequence 3, Appli
8	938.5	41.2	1655	12	US-09-794-422-1	Sequence 1, Appli
9	148.5	6.5	8201	12	US-10-363-798-1	Sequence 1, Appli
10	148	6.5	5721	10	US-09-785-770A-15	Sequence 15, Appl
11	148	6.5	8121	10	US-09-785-770A-14	Sequence 14, Appl
12	140	6.1	2673	14	US-10-153-668-301	Sequence 301, App
13	140	6.1	4839	12	US-10-101-510-398	Sequence 398, App
14	139	6.1	35465	14	US-10-161-572-6	Sequence 6, Appli
15	139	6.1	36991	14	US-10-161-572-8	Sequence 8, Appli
16	137	6.0	9390	14	US-10-205-823-263	Sequence 263, App
17	134.5	5.9	4084	13	US-10-153-273-1	Sequence 1, Appli
18	134	5.9	1446	14	US-10-156-761-4465	Sequence 4465, Ap
19	134	5.9	2254	14	US-10-198-846-13929	Sequence 13929, A
20	134	5.9	9025608	14	US-10-156-761-1	Sequence 1, Appli
21	133.5	5.9	1960	9	US-09-864-761-4620	Sequence 4620, Ap
22	133.5	5.9	7058	12	US-10-287-218-38	Sequence 38, Appl
23	131	5.7	2025	10	US-09-834-975-822	Sequence 822, App
24	130.5	5.7	1450	13	US-10-001-835-66	Sequence 66, Appl
25	130.5	5.7	3316	12	US-10-133-013-166	Sequence 166, App
26	130.5	5.7	5469	12	US-10-341-434-94	Sequence 94, Appl
27	130	5.7	1501	12	US-10-017-161-2097	Sequence 2097, Ap
28	129.5	5.7	2454	9	US-09-962-436-563	Sequence 563, App
29	129.5	5.7	2454	14	US-10-175-523-55	Sequence 55, Appl
30	129.5	5.7	2480	14	US-10-060-036-4548	Sequence 4548, Ap
31	129.5	5.7	2491	14	US-10-084-817-352	Sequence 352, App
32	129.5	5.7	2885	14	US-10-198-846-13303	Sequence 13303, A
33	127.5	5.6	1763	12	US-10-017-161-2323	Sequence 1, Appli
34	127.5	5.6	3708	12	US-09-758-036-1	Sequence 3423, Ap
35	127.5	5.6	4840	10	US-09-880-107-3423	Sequence 63, Appl
36	127	5.6	1066	11	US-09-746-660A-63	Sequence 2161, Ap
37	127	5.6	2154	10	US-09-738-626-2161	Sequence 22571, A
38	127	5.6	2612	12	US-10-029-386-22571	Sequence 253, App
39	127	5.6	2636	14	US-10-153-668-253	Sequence 295, App
40	127	5.6	4215	14	US-10-037-270-295	Sequence 29, Appl
41	127	5.6	4380	12	US-10-094-466-29	Sequence 6, Appli
42	127	5.6	5331	10	US-09-764-176-6	Sequence 188, App
43	127	5.6	11167	12	US-10-252-157-188	Sequence 1, Appli
44	127	5.6	3309400	10	US-09-738-626-1	Sequence 1739, Ap
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ALIGNMENTS

RESULT 1
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; Sequence 2, Application US/10311840
; Publication No. US20030175808A1
; GENERAL INFORMATION:
; APPLICANT: KUROKAWA, Tomofumi
; APPLICANT: YAMADA, Takao
; APPLICANT: MORIMOTO, Shigetomo
; TITLE OF INVENTION: No. US20030175808A1 Protein and its DNA
; FILE REFERENCE: 2738USOP
; CURRENT APPLICATION NUMBER: US/10/311,840
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: PCT/JP01/05263
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: JP 2000-191088
; PRIOR FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 2
; LENGTH: 1575
; TYPE: DNA
; ORGANISM: Human
US-10-311-840-2

Score: 2276.00 Matches: 429
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.77% Mismatches: 0
Query Match: 99.87% Indels: 0
DB: 12 Gaps: 0

US-09-700-696C-2 (1-430) x US-10-311-840-2 (1-1575)

Qy 1 ValAsnLysGluTyrSerIleSerAsnLysGluAsnThrHisAsnGlyLeuArgMetSer 20
Db 286 CTGAATAAAGAAATATAGTATCAGTAACAAAGAGAAATCTCACAATGGCTGAGGATGTCA 345

Qy 21 IleTyrProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerLys 40
Db 346 ATTTATCTCAAGTCAACTGGGAAATAAAGGGTTTGGAGATGGAGATGCTATCAGCAA 405

Qy 41 LeuHisAspGlnGluTyrGlyAlaAlaLeuIleArgAsnMetGlnHisIleMet 60
Db 406 CTACATGACCAAGAAGAAATATGGCGAGCTCTCATCAGAAATACATGCAACATATATG 465

Qy 61 GlyProValThrAlaIleLysLeuGlyGluGluAsnLysGluAsnThrProArgAsn 80
Db 466 GGGCCAGTGTGCGATTAACTCTCTGGGGAGAAACAAAGAGAAACACACCTTAGGAAT 525

Qy 81 ValLeuAsnIleIleProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLys 100
Db 526 GTTCTAAACATAATCCAGCAGATGATGATATATCTAAAGCACACTCGAAGGATAAAAG 585

Qy 101 LysProGlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArg 120
Db 586 AAGCCTCAAGAGATTTCCCAAGCCAGAAAAGTCCAGTAAAGCAAAAGCAACCATCGT 645

Qy 121 IleGlnHisAsnIleAspTyrLeuLysHisLeuSerLysValLysLysIleProSerAsp 140
Db 646 ATTCAACACACAATGACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 705

Qy 141 PheGluGlySerGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPhe 160
Db 706 TTGTGAAGGACGGTTTATACAGATCTTCAAGAGAGAGGAGCAATGATATATCTCTCTTC 765

Qy 161 SerGlyAspGlyGlnProPheLysAspIleProGlyLysGlyGluAlaThrGlyProAsp 180
Db 766 AGTGGGACGCGCAACCTTTAAGGACATCTCTGTAAAGAGAGAGTACTGTGCTCTGAC 825

Qy 181 LeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHis 200
Db 826 CTGAAGGCAAGATATTCACACAGGGTTTGCAGGCCCAAGTGAAGCTGAGAGTACTCAT 885

Qy 201 LeuAspThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsn 220
Db 886 CTTGACACAAAAGCCAGGTTTATATGAGATCCAGAGAGAGAAATGGTGGAAAT 945

Qy 221 ThrIleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuVal 240
Db 946 ACCATTGGAACTAGGATGAACTGCGAAAGAGCGAGATGCTGTGATGTGACCTTTGTA 1005

Qy 241 GluGlySerAsnAspIleMetGlySerThrAsnPhelysGluLeuProGlyArgGluGly 260
Db 1006 GAGGGCAGCAACCATATCTGGGTAGTACCATAATTTAAGAGAGTCCCTGGAAGAGAAGGA 1065

Qy 261 AsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrPro 280
Db 1066 AACAGAGTGTGATCTGGCAGCAAAATGCTCACCAGGGAGAGTTGAGTTTCTATTACCT 1125

Qy 281 ProAlaProSerLysGluLysArgLysGluGlySerSerAspAlaAlaGluSerThrAsn 300
Db 1126 CCTGCACTCTCAAAAGAGAAAGAAAGAGAGGAGGAGTGTGATGAGTGAAGTACCAAC 1185

Qy 301 TyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsn 320
Db 1186 TATATGAATTTCTTAAATATGCAAGGAGGAGTACCAGAAAGGGTGTAGATCATTTCTAAT 1245

Qy 321 ArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGly 340

Db 1246 AGGAACCAAGCACCTTAAATGAAAAACAAAGGTTTCTAGTAAGGGCAAAAGTCAGGCG 1305

Qy 341 LeuProIleProSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsn 360
Db 1306 CTGCCCATTCCTCTCTGGTGTCTTGAATAAGAAATCAAAACGAAATGGATTCCTTAAAT 1365

Qy 361 GlyProSerHisGluAsnIleIleThrHisGlyArgLysTyrHisTyrValProHisArg 380
Db 1366 GGCCCCAGTCATGAGATATAATAACACATGGCAGAAAAATATCATTTATGATACCCACAGA 1425

Qy 381 GlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySerTrpGlyArgGln 400
Db 1426 CAAAATAATTTCTACACGGAATAAGGGTATGCGCAACAGGAAAGGCTCTCTGGGGTAGACA 1485

Qy 401 ProHisSerAsnArgArgPheSerSerArgArgAspAspSerSerGluSerSerAsp 420
Db 1486 CCCCATTTCCACAGAGAGTTTGTTCCTCCGTAGAGGGATGACAGTAGTGTCTCATCTGAC 1545

Qy 421 SerGlySerSerGluSerAspGlyAsp 430
Db 1546 AGTGGCAGTTTCAAGTGAGAGCGATGTTGAC 1575

RESULT 2
US-10-311-840-3
; Sequence 3, Application US/10311840
; Publication No. US20030175808A1
; GENERAL INFORMATION:
; APPLICANT: KUROKAWA, Tomofumi
; APPLICANT: YAMADA, Takao
; APPLICANT: MORIMOTO, Shigeto
; TITLE OF INVENTION: No. US20030175808A1 Protein and its DNA
; FILE REFERENCE: 2738USOP
; CURRENT APPLICATION NUMBER: US/10/311,840
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: PCT/JP01/05263
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: JP 2000-191088
; PRIOR FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 3
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Human
US-10-311-840-3

Alignment Scores:
Pred. No.: 2,38e-213 Length: 1662
Score: 2276.00 Matches: 429
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.77% Mismatches: 0
Query Match: 99.87% Indels: 0
DB: 12 Gaps: 0

US-09-700-696C-2 (1-430) x US-10-311-840-3 (1-1662)

Qy 1 ValAsnLysGluTyrSerIleSerAsnLysGluAsnThrHisAsnGlyLeuArgMetSer 20
Db 293 CTGAATAAAGAAATATAGTATCAGTAACAAAGAGAAATCTCACAATGGCTGAGGATGTCA 352

Qy 21 IleTyrProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerLys 40
Db 353 ATTTATCTCAAGTCAACTGGGAAATAAAGGGTTTGGAGATGGAGATGATGCTATCAGCAA 412

Qy 41 LeuHisAspGlnGluTyrGlyAlaAlaLeuIleArgAsnMetGlnHisIleMet 60
Db 413 CTACATGACCAAGAAGAAATATGGCGAGCTCTCATCAGAAATACATGCAACATATAATG 472

Qy 61 GlyProValThrAlaIleLysLeuGlyGluGluAsnLysGluAsnThrProArgAsn 80
Db 473 GGGCCAGTGTGCGATTAACTCTCTGGGGAGAAACAAAGAGAGACACACCTTAGGAAT 532

Qy 81 ValLeuAsnIleIleProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLys 100

Db 533 GTTCTAAACATAATCCAGCAAGTATGAAATATGCTAAAGCACATCGAAGGATAAAAG 592
Qy 101 LysProGlnArgAspSerGlnAlaGlnLysSerProValLysSerLysThrHisArg 120
Db 593 AAGCCTCAAGAGATCCCAAGCCCAAGAAAGTCCAGTAAAGCAAGCAAGCAAGCAAGTGT 552
Qy 121 IleGlnHisAsnIleAspTyrLeuLysHisLeuSerLysValLysLysIleProSerAsp 140
Db 653 ATTCAACACACATGACTACCTACCTAAACATCTCTCAAAAGTCAAAATAATCCCAAGTAT 712
Qy 141 PheGluGlySerGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPhe 160
Db 713 TTTGAAGCGACGGTTATACAGATCTTCAAGAGAGAGGGGACCAATGATATATCTCTCTTC 772
Qy 161 SerGlyAspGlyGlnProPheLysAspIleProGlyLysGlyGluAlaThrGlyProAsp 180
Db 773 AGTGGGACGGCCACCTTTTAGGACATCTCTGGTAAAGGAGAGCTACTGCTCTGAC 832
Qy 181 LeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHis 200
Db 833 CTAGAGGCAAGATATCAACAGAGGTTTGCAGGCCCAAGTGAAGCTGAGAGTACTCAT 892
Qy 201 LeuAspThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsn 220
Db 893 CTTGACACAAAAGCCAGGTTATATGAGATCCAGAGAGAGAGAAATGGTGGAAAT 952
Qy 221 ThrIleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValSerLeuVal 240
Db 953 ACCATTGGAACTAGGATGAACTGCGAAAGAGGACAGTCTGTGTGATGTGACCTTGTA 1012
Qy 241 GluGlySerAsnAspIleMetGlySerThrAsnPhelLysGluLeuProGlyArgGluGly 260
Db 1013 GAGGGCAGCAAGATATCATGCTGGTGTAGTACCAATTTTAAAGAGCTCCCTGGAAGAGAGGA 1072
Qy 261 AsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrPro 280
Db 1073 AACAGATGGATGCTGGCAGCCAAATGCTCACCAGCGAAGGTGTGATTTCTATCCCT 1132
Qy 281 ProAlaProSerLysGluLysArgLysGluGlySerSerAspAlaAlaGluSerThrAsn 300
Db 1133 CCTGACCCCTCAAAAGAGAGAAAGAAAGAGGCGATAGTATGATGAGCTGAAGTACCAAC 1192
Qy 301 TyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsn 320
Db 1193 TATATATGAAATCTTAAATATGCAAGGCGATGACCAAGAGGTGTAGATCATTTCTAT 1252
Qy 321 ArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGly 340
Db 1253 AGGAACCAAGCAACCTTAAATGAAACAAAGGTTTCTAGTAAAGGCAAAAGTCAGGGC 1312
Qy 341 LeuProIleProSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsn 360
Db 1313 CTGCCCATCTCTCTGCTGTGATATGAAATCAAAACGAAATGGATTCCTTTAT 1372
Qy 361 GlyProSerHisGluAsnIleThrHisGlyArgLysTyrHisTyrValProHisArg 380
Db 1373 GGCCCCAGTCATGAGATATAATAACATGCCAGAAAAATATCATTTATGATACCCACAGA 1432
Qy 381 GlnAsnAsnSerThrArgAsnLysGlyMetProGlnLysGlySerThrGlyArgGln 400
Db 1433 CAAATAATCTACAGGAATTAAGGATGTCACAGGGGAAAGGCTCCTGGGGTAGACAA 1492
Qy 401 ProHisSerAsnArgPheSerSerArgArgAspAspSerSerGluSerSerAsp 420
Db 1493 CCCCATTTCAACAGAGGTTTGTAGTTCCCGTAGAGGGATGACATGATGATCATCTGAC 1552
Qy 421 SerGlySerSerGluSerAspGlyAsp 430
Db 1553 AGTGCGAGTTCAAGTGAAGGCGATGGTAC 1562
RESULT 3
US-09-794-422-33

; Sequence 33, Application US/09794422
; Publication NO. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PCI0445
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-794-422-33
Alignment Scores:
Pred. No.: 2,78e-213 Length: 1876
Score: 2276.00 Matches: 429
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.77% Mismatches: 0
Query Match: 99.87% Indels: 0
DB: 12 Gaps: 0
US-09-700-696C-2 (1-430) x US-09-794-422-33 (1-1876)

Qy 1 ValAsnLysGluTyrSerIleSerAsnLysGluAsnThrHisAsnGlyLeuArgMetSer 20
Db 238 CTGAATAAAGATATAGTATAGTAAACAAGAGATACTCAATGGGCTGAGGATGTCA 297
Qy 21 IleTyrProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerLys 40
Db 298 ATTATCTTAACTCACTGGGAAATAAAGGTTTGAAGTGGAGATGATGCTATCAGCAA 357
Qy 41 LeuHisAspGlnGluTyrGlyAlaAlaLeuIleArgAsnAsnMetGlnHisIleMet 60
Db 358 CTACATGACCAAGAAGATATGGCGAGCTCTCATCAGAAATAACATGCAACATATAATG 417
Qy 61 GlyProValThrAlaIleLysLeuLeuGlyGluGluAsnLysGluAsnThrProArgAsn 80
Db 418 GGGCCAGTGACTGCGATTAAACTCTCTGGGGGAGAAACAAAGAGAACACACCTTAGGAAT 477
Qy 81 ValLeuAsnIleIleProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLys 100
Db 478 GTTCTAAACATATCCAGCAAGTATGAAATTATGCTAAAGCACACTCGAAGGATAAAAG 537
Qy 101 LysProGlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArg 120
Db 538 AAGCCTCAAGAGATTCCTCAAGCCCAAGAAAGTCCAGTAAAGCAAAAGCAAGCACCATCGT 597
Qy 121 IleGlnHisAsnIleAspTyrLeuLysHisLeuSerLysValLysLysIleProSerAsp 140
Db 598 ATTCAACACACATTTGACTACTTAAACATCTCTCAAAAGTCAAAATAATCCCAAGTAT 657
Qy 141 PheGluGlySerGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPhe 160
Db 658 TTTGAAGCGACGGTTATACAGATCTTCAAGAGAGAGGGGACCAATGATATATCTCTTTC 717
Qy 161 SerGlyAspGlyGlnProPheLysAspIleProGlyLysGlyGluAlaThrGlyProAsp 180
Db 718 AGTGGGACGGCCAACTTTTAAAGACATCTCTGTTAAAGGAGAGAGCTACTGGTCTCTGAC 777
Qy 181 LeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHis 200
Db 778 CTAGAGGCAAGATATTCAAACAGGGTTTGCAGGCCCAAGTGAAGCTGAGAGTACTCAT 837

QY 201 LeuAspThrLysLysProGlyTyrAsnGluLeuProGluArgGluGluAsnGlyGlyAsn 220
DB 838 CTTGACACAAAAAGCCAGGTATAATGAGATCCAGAGAGAGAGAAATGGTGAAT 897
QY 221 ThrIleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValSerLeuVal 240
DB 898 ACCATTGGAACTAGGATGAACCTGCGAAGAGGAGCATGCTGTTGATGACGCTTGTGA 957
QY 241 GluGlySerAsnAspIleMetGlySerThrAsnPhelLysGluLeuProGlyArgGluGly 260
DB 958 GAGGGCAGCAACGATATCATGGGTAGTACCAATTTTAAGGAGCTCCCTGGAGAGAGGA 1017
QY 261 AsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrPro 280
DB 1018 AACAGAGTGTGATGCTGCAGCCCAAAATGCTCACCAAGGGAAGGTGTGATTTTCATTACCT 1077
QY 281 ProAlaProSerLysGluLysArgLysGluGlySerSerAspAlaAlaGluSerThrAsn 300
DB 1078 CTTGCACCTCAGAGAGAAAGAAAGAGAGGCGTGTAGTGCAGCTGAAGTACCAC 1137
QY 301 TyrAsnGluLeuProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsn 320
DB 1138 TATAATGAATTCCTAAAAATGGCAAGGCGAGTACCAGAAAGGTGTAGATCATTTCTAAT 1197
QY 321 ArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGly 340
DB 1198 AGAACCAACCAACCTTAAATGAAACAAAGGTTTCTAGTAAAGGCAAAAGTCAGGGC 1257
QY 341 LeuProIleProSerArgGlyLeuAspAsnGluLeuLysAsnGluMetAspSerPheAsn 360
DB 1258 CTGCCCATCTCTTCGTGCTTGATAATGAATCAAAACGAAATGGATTCCTTTAAT 1317
QY 361 GlyProSerHisGluAsnIleIleThrHisGlyArgLysTyrHisTyrValProHisArg 380
DB 1318 GGCCCCAGTCATGAGATATAATTAACACATGGCAGAGAAATATCATTTATGTACCCACAGA 1377
QY 381 GlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySerTyrGlyArgGln 400
DB 1378 CAAAAATATCTACACGGAATAAGGTATGCCAAGGGAAAGGCTCCTGGGGTAGACAA 1437
QY 401 ProHisSerAsnArgPheSerSerArgArgAspAspSerSerGluSerSerAsp 420
DB 1438 CCCCATTCACACAGGAGTTTGTCTCCGTAGAAGGATGACAGTAGTCAATCTGAC 1497
QY 421 SerGlySerSerGluSerAspGlyAsp 430
DB 1498 AGTGGCAGTTCAGAGTGAAGCGATGTGAC 1527

RESULT 4

US-09-794-422-45
; Sequence 45, Application US/09794422
; Publication No. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PCI0445
; CURRENT APPLICATION NUMBER: US/09/794,422
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 1969
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-794-422-45

Alignment Scores:

Pred. No.: 2,96e-213 Length: 1969
Score: 2276.00 Matches: 429
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.77% Mismatches: 0
Query Match: 99.87% Indels: 0
DB: 12 Gaps: 0

US-09-700-696C-2 (1-430) x US-09-794-422-45 (1-1969)

QY 1 ValAsnLysGluTyrSerIleSerAsnLysGluAsnThrHisAsnGlyLeuArgMetSer 20
DB 331 CTGATAAAGAAATATAGTATCAGTAAACAAAGAGAAATACTCACATGGCTCAGCATGTCA 390
QY 21 IleTyrProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerLys 40
DB 391 ATTATTCCTAAGTCACTGGGAATAAAGGTTTGAAGATGGAGATGATGCTATCAGCAA 450
QY 41 LeuHisAspGlnGluTyrGlyAlaAlaLeuIleArgAsnAsnMetGlnHisIleMet 60
DB 451 CTACATGACCACAGAGAAATATGGCGAGCTCTCATCAGAAATAACATGCAACATATAATG 510
QY 61 GlyProValThrAlaIleLysLeuLeuGlyGluGluAsnLysGluAsnThrProArgAsn 80
DB 511 GGCCCGAGTGACTCGGATTAAACTCCTGGGGGAAAGAAACAAAGAGAACACACCTAGGAAT 570
QY 81 ValLeuAsnIleIleProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLys 100
DB 571 GTTCTAAACATATCCAGCAGATGATGAATATGCTTAAGCACACTCGAAGGATAAAG 630
QY 101 LysProGlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArg 120
DB 631 AAGCCTCAAGAGATTCCTCAAGCCAGAAAAGTCCAGTAAAAAGCAAAACACCCATCGT 690
QY 121 IleGlnHisAsnIleAspTyrLeuLysHisLeuSerLysValLysLysIleProSerAsp 140
DB 691 ATTCAACACAAACATTCACCTACCTAAACATCTCTCAAAAGTCAAAAATAATCCCCAGTAT 750
QY 141 PheGluGlySerGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPhe 160
DB 751 TTTGAAGGACGCGTTATACAGATCTTCAAGAGAGAGGGACAAATGATATATCTCTCTTC 810
QY 161 SerGlyAspGlyGlnProPheLysAspIleProGlyLysGlyGluAlaThrGlyProAsp 180
DB 811 AGTGGGACGGCCCAACCTTTTAAGGACATTCCTGGTAAAGAGAGAGCTACTGGTCTGAC 870
QY 181 LeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHis 200
DB 871 CTAGAAGGCAAAAGATATTCAACAGGGTTTGCAGGGCCCAAGTGAAGCTGAGAGTACTCAT 930
QY 201 LeuAspThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsn 220
DB 931 CTTGACACAAAAAGCCAGGTATAATGAGATCCAGAGAGAGAGAAATATGGTGAAT 990
QY 221 ThrIleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValSerLeuVal 240
DB 991 ACCATTGGAACCTAGGATGAAACTCGAAAAGAGGCGAGATGCTGTTGATGTCAGCCCTGTA 1050
QY 241 GluGlySerAsnAspIleMetGlySerThrAsnPhelLysGluLeuProGlyArgGluGly 260
DB 1051 GAGGGCAGCAACGATATCATGGGTAGTACCAATTTTAAGGAGCTCCTCGAAGAGAGGA 1110
QY 261 AsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrPro 280
DB 1111 AACAGAGTGTGCTGGCAGCCAAATGCTCACCAAGGGAAGGTGTGAGTTTCATTACCT 1170
QY 281 ProAlaProSerLysGluLysArgLysGluGlySerSerAspAlaAlaGluSerThrAsn 300
DB 1171 CCTGCACCTCAGAGAGAAAGAAAGAGGCGATGTAGTGTGACGTGAAAGTACCAC 1230
QY 301 TyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsn 320
DB 1231 TATAATGAATTCCTAAAAATGGCAAGGCGATGACCAAGAAAGGGTGTAGATCATTTCTAAT 1290


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QY 321 ArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGly 340
Db 1291 AGGAACCAAGCAACCTTAAATGAAACAAAGGTTTCTAGTAAGGCAAAAGTCAGGC 1350
QY 341 LeuProIleProSerArgGlyLeuAspAsnGluLysAsnGluMetAspSerPheAsn 360
Db 1351 CTGCCCATCTCTCTCTGCTGCTTGAATGAATCAAAACGAAATGGATTCCTTTAAT 1410
QY 361 GlyProSerHisGluAsnIleIleThrHisGlyArgLysTyrHisTyrValProHisArg 380
Db 1411 GGCCCCAGTCATGAGATATAATAACACATGGCAGAAATATCATTTATGTACCCACAGA 1470
QY 381 GlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySerTrpGlyArgGln 400
Db 1471 CAAAAATAATTCACAGGAATAAGGGTATGCCCAAGGGAAGGCTCTCTGGGTAGACAA 1530
QY 401 ProHisSerAsnArgPheSerSerArgArgArgAspAspSerSerGluSerSerAsp 420
Db 1531 CCCCATTCACACAGGAGGTTTACTTCCCGTAGAAGGATGACAGTAGTAGTCACTCTGAC 1590
QY 421 SerGlySerSerSerGluSerAspGlyAsp 430
Db 1591 AGTGGCAGTTCAAGTGAGAGCGATGGTGAC 1620

RESULT 5
US-09-794-422-5
; Sequence 5, Application US/09794422
; Publication No. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-794-422-5

Alignment Scores:
Pred. No.: 3,06e-213 Length: 2019
Score: 2276.00 Matches: 429
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.77% Mismatches: 0
Query Match: 99.87% Indels: 0
DB: 12 Gaps: 0

US-09-700-696C-2 (1-430) x US-09-794-422-5 (1-2019)

QY 1 ValAsnLysGluTyrSerIleSerAsnLysGluAsnThrHisAsnGlyLeuArgMetSer 20
Db 381 CTGAATAAAGATATAGTATCATCAACAAAGAGATACTCAATGGCCCTGAGGATGTCA 440
QY 21 IleTyrProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerLys 40
Db 441 ATTTATCTCAAGTCAACTCGGAATAAAGGTTTGAAGATGGAGATGCTATCAGCAA 500
QY 41 LeuHisAspGlnGluGluTyrGlyAlaLeuIleArgAsnMetGlnHisIleMet 60
Db 501 CTACATGACCAAGAGAAGATATGGCGAGCTCTCATCAGAAATAACATGCAACATATAATG 560
QY 61 GlyProValThrAlaIleLysLeuLeuGlyGluGluAsnLysGluAsnThrProArgAsn 80
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Db 561 GGCCCAAGTGACTCGGATTAAACTCTCTGGGGGAAGAAACAAAGAGAACACACCTTAGGAAT 620
QY 81 ValLeuAsnIleIleProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLys 100
Db 621 GTTCTAAACATATATCCAGCAAGTATGAATATGCTAAAGCACACTCGAAGGATAAAAG 680
QY 101 LysProGlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArg 120
Db 681 AAGCCTCAAGAGATTCCTCAAGCCAGAAAAGTCCAGTAAAAAGCAAAAGCACCATCGT 740
QY 121 IleGlnHisAsnIleAspTyrLeuLysHisLeuSerLysValLysLysIleProSerAsp 140
Db 741 ATTCAACACACAACTGACTACCTTAAACCATCTCTCAAAAGTCAAAAAAATCCCCAGTAT 800
QY 141 PheGluGlySerGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPhe 160
Db 801 TTTGAAGGCAGCGGTTATACAGATCTTCAGAGAGAGGGGACATGATATATCTCTCTTTC 860
QY 161 SerGlyAspGlyGlnProPheLysAspIleProGlyLysGlyGluAlaThrGlyProAsp 180
Db 861 AGTGGGAGCGGCCAACCTTTTAAAGGACATTCCTGGTAAAGAGAGAGCTACTGGTCTTGAC 920
QY 181 LeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHis 200
Db 921 CTAGAAGGCAGGAGATATTCAAACAGGGTTTGCAGGCCCAAGTGAAGCTGAGAGTACTCAT 980
QY 201 LeuAspThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsn 220
Db 981 CTTGACACAAAAAGCCAGGTTATATGAGATCCACAGAGAGAGAGAAATGTTGGAAT 1040
QY 221 ThrIleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuVal 240
Db 1041 ACCATTGGAACTAGGATGAACTGCGAAAGAGGAGAGATGCTCTGTATGTCAGCCTTGT 1100
QY 241 GluGlySerAsnAspIleMetGlySerThrAsnPheLysGlnLeuProGlyArgGluGly 260
Db 1101 GAGGGCAGACAGATATCATGGGTAGTACCAATTTTAAAGGAGCTCCCTGGAAGAGGA 1160
QY 261 AsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyValGluPheHisTyrPro 280
Db 1161 AACAGATGGATGCTGCGACCCAAAATGCTCACCAAGGGAAGGTTGAGTTTCAATACCT 1220
QY 281 ProAlaProSerLysGluLysArgLysGluLysSerSerAspAlaAlaGluSerThrAsn 300
Db 1221 CCTGCACCTCAAAAGAGAAAGAAAGAGGAGGAGTGTGATGTCAGCTGAAAGTACCAAC 1280
QY 301 TyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsn 320
Db 1281 TATAATGAAATTCCTTAAAAATGCAAGGAGTACCAGAAAGGCTGTAGATCATCTTAAT 1340
QY 321 ArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGly 340
Db 1341 AGGAACCAAGCAACCTTAAATGAAACAAAGGTTTCTAGTAAGGCAAAAGTCAGGC 1400
QY 341 LeuProIleProSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsn 360
Db 1401 CTGCCCATCTCTCTGCTTGAATAATGAAATCAAAACGAAATGGATTCCTTTAAT 1460
QY 361 GlyProSerHisGluAsnIleIleThrHisGlyArgLysTyrHisTyrValProHisArg 380
Db 1461 GGCCCCAGTCATGAGATATAATAACATGGCAGAAATATCATTTATGTACCCACAGA 1520
QY 381 GlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySerTrpGlyArgGln 400
Db 1521 CAAATATATTCACAGGATTAAGGTTATGCCCAAGGGAAGGCTCTCTGGGGTAGACAA 1580
QY 401 ProHisSerAsnArgPheSerSerArgArgArgAspAspSerSerGluSerSerAsp 420
Db 1581 CCCCATTCCACAGGAGGTTTAGTTCCCGTAGAAGGATGACAGTAGTAGTCACTCTGAC 1640
QY 421 SerGlySerSerSerGluSerAspGlyAsp 430
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Db	1641	AGTGGCAGTTCAAGTGAGGCGATGGTGAC	1670
RESULT 6			
US-09-794-422-7			
; Sequence 7, Application US/09794422			
; Publication No. US20030166239A1			
; GENERAL INFORMATION:			
; APPLICANT: Brown, Thomas A.			
; APPLICANT: De Wet, Jeffrey R.			
; APPLICANT: Gowen, Lori C.			
; APPLICANT: Hames, Lynn M.			
; TITLE OF INVENTION: Mammalian Osteoregulins			
; FILE REFERENCE: PC10445			
; CURRENT APPLICATION NUMBER: US/09/794,422			
; CURRENT FILING DATE: 2001-02-27			
; PRIOR APPLICATION NUMBER: 60/185,617			
; PRIOR FILING DATE: 2000-02-29			
; PRIOR APPLICATION NUMBER: 60/234,500			
; PRIOR FILING DATE: 2000-09-22			
; NUMBER OF SEQ ID NOS: 46			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 7			
; LENGTH: 2112			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-09-794-422-7			
Alignment Scores:			
Pred. No.: 3,25e-213 Length: 2112			
Score: 2276.00 Matches: 429			
Percent Similarity: 100.00% Conservative: 1			
Best Local Similarity: 99.77% Mismatches: 0			
Query Match: 99.87% Indels: 0			
DB: 12 Gaps: 0			
US-09-700-696c-2 (1-430) x US-09-794-422-7 (1-2112)			
QY	1	ValAsnLysGluTyrSerIleSerAsnLysGluAsnThrHisAsnGlyLeuArgMetSer	20
Db	474	CTGAATAAAGATATAGTATCATCAACAAAGAGATATCTCAATGGCTGAGGATGTCA	533
QY	21	IleTyrProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAspAlaIleSerLys	40
Db	534	ATTATCTCACTAAGTCACTGGGATAAAGGTTTGAGGATGGAGATGCTATCAGCAA	593
QY	41	LeuHisAspGlnGluTyrGlyAlaIleAlaLeuIleArgAsnAsnMetGlnHisIleMet	60
Db	594	CTACATGACCAAGAAGATATGGCGAGCTCTCATCAGAAATAACATGCAACATATAATG	653
QY	61	GlyProValThrAlaIleLysLeuLeuGlyGluAsnLysGluAsnThrProArgAsn	80
Db	654	GGGCCAGTGACTGGGATTAACCTCTGGGGGAAGAAACAAAGAGAACACACCTAGGAAT	713
QY	81	ValLeuAsnIleIleProIleSerMetAsnTyrAlaLysAlaHisSerLysAspLysLys	100
Db	714	GTCTAAACATATCCCAAGATATGAATTAATGCTAAAGCACATCGAAGGATAAAAG	773
QY	101	LysProGlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArg	120
Db	774	AGGCTCAAGAGATTCACAGCCCAAGAAAGTCCAGTAAAGCAAAAGCACCCATCGT	833
QY	121	IleGlnHisAsnIleAspTyrLysLysHisLeuSerLysValLysLysIleProSerAsp	140
Db	834	ATTCAACACAACTTACTACCTCAAAACATCTCTCAAAAGTCAAAAAATCCCAAGTAT	893
QY	141	PheGluGlySerGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPhe	160
Db	894	TTTGAAGGCGCGGTTATACAGATCTTCAAGAGAGAGGGGACATGATATATCTCTCTTC	953
QY	161	SerGlyAspGlyGlnProPheLysAspIleProGlyLysGlyGluAlaThrGlyProAsp	180
Db	954	AGTGGGCGCGCCCACTTTTAAGGACATCTCTGGTTAAAGGAGAGAGTACTGCTCTCTGAC	1013
QY	181	LeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHis	200
Db	1014	CTAGAAGGCAAGAATATTCAAAACAGGTTTGAGGCCCCCAAGTGAAGCTGAGAGTACTCAT	1073
QY	201	LeuAspThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsn	220
Db	1074	CTTGACACAAAAAGCCAGGTTTATATGAGATCCCAAGAGAGAGAAATATGGTGGAAAT	1133
QY	221	ThrIleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuVal	240
Db	1134	ACCATTTGGACTAGGATGAATCTCGAAAGAGGCGAGATGCTGTTGATGTGACCTTGTA	1193
QY	241	GluGlySerAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGly	260
Db	1194	GAGGGCAGCAACGATATCATGGGTATGATCAATTTTAAGGAGCTCCCTGGAGAGAGAA	1253
QY	261	AsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrPro	280
Db	1254	ACAGAGTGGATGCTGGCAGCCAAATGCTCCCAAGGAGGAGTTGAGTTTCATTACCT	1313
QY	281	ProAlaProSerLysGluLysArgLysGluGlySerSerAspAlaAlaGluSerThrAsn	300
Db	1314	CCTGCACCTCAAAAGAGAGAAAGAAAGAGGAGTGTGATGATGATGATGATGATGATGAT	1373
QY	301	TyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsn	320
Db	1374	TATAATGAATTTCTTAAATGCAAGGAGTATCCAGAAAGGAGTGTAGTATCATTTAAT	1433
QY	321	ArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGly	340
Db	1434	AGGAACCAAGCAACCTTAAATGAAAAACAAAGTTTCCTAGTAAGGCGCAAAAGTCAGGC	1493
QY	341	LeuProIleProSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsn	360
Db	1494	CTGCCCATTCCTCTCTGCTTGAATGATAATGAAATCAAAAGCAAAATGATTCCTTAAT	1553
QY	361	GlyProSerHisGluAsnIleIleThrHisGlyArgLysTyrHisTyrValProHisArg	380
Db	1554	GGCCCCAGTCAGAGATATATAACACATGGCAGAAATAATCATTTATGTACCCACAGA	1613
QY	381	GlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySerTrpGlyArgGln	400
Db	1614	CAAAATAATTTACACGGAATAGGTTATGCCCAAGGGAAGGCTCTCTGGGGTAGACAA	1673
QY	401	ProHisSerAsnArgPheSerSerArgArgArgAspAspSerGluSerSerAsp	420
Db	1674	CCCATTTCCAAAGAGGAGTTTATTTCCCTAGAGAGGATGACAGTATGATGATCTGAC	1733
QY	421	SerGlySerSerSerGluSerAspGlyAsp	430
Db	1734	AGTGGCAGTTTCAAGTGAGGCGATGCTGAC	1763
RESULT 7			
US-09-794-422-3			
; Sequence 3, Application US/09794422			
; Publication No. US20030166239A1			
; GENERAL INFORMATION:			
; APPLICANT: Brown, Thomas A.			
; APPLICANT: De Wet, Jeffrey R.			
; APPLICANT: Gowen, Lori C.			
; APPLICANT: Hames, Lynn M.			
; TITLE OF INVENTION: Mammalian Osteoregulins			
; FILE REFERENCE: PC10445			
; CURRENT APPLICATION NUMBER: US/09/794,422			
; CURRENT FILING DATE: 2001-02-27			
; PRIOR APPLICATION NUMBER: 60/185,617			
; PRIOR FILING DATE: 2000-02-29			
; PRIOR APPLICATION NUMBER: 60/234,500			
; PRIOR FILING DATE: 2000-09-22			
; NUMBER OF SEQ ID NOS: 46			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 3			
; LENGTH: 1682			

TYPE: DNA			
ORGANISM: Mus musculus			
US-09-794-422-3			
Alignment Scores:			
Pred. No.:	1.06e-86	Length:	1682
Score:	983.50	Matches:	217
Percent Similarity:	62.56%	Conservative:	52
Best Local Similarity:	50.47%	Mismatches:	134
Query Match:	43.15%	Indels:	27
DB:	12	Gaps:	8
US-09-700-696C-2 (1-430) x US-09-794-422-3 (1-1682)			
QY	6 SerIleSerAsnLysGluAsnThrHisAsnGlyLeuArgMetSerIleTyrProLysSer 25		
DB	166 AGCTGGCGCATCAAGACAGCATTCACAAAGACTTGGCAGCATCTGTGTATCTGTATCC 225		
QY	26 ThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerLysLeuHisAspGlnGlu 45		
DB	226 ACCGTGATGAAGGCACAGAGGATGGCAAGGTCTCTCTTCCACCGCTGGCCAGGAC 285		
QY	46 GluTyrGlyAlaAlaIleAtrGAsnAsnMetGlnHisIleMetGlyProValThrAla 65		
DB	286 AGGTATGTCCTGCTCTCTCCAGAAATATCAGCGAGCTGTAAAGACTGTAGTACTGG 345		
QY	66 IleLysLeuLeuGlyGluAsnLysGluAsnThrProArgAsnValLeuAsnIle 85		
DB	346 GCCGAACCTACGGAGGGAAGAAACCCAGAGAGACCTCAGAGTGTCTTAAGCGTAATT 405		
QY	86 ProIleSerMetAsnTyrAlaLysAlaHisSerLysAspLysLysProGlnArgAsp 105		
DB	406 CCAGCAGATGCAATGATGCTAAAGTCTCTTAAGACATAAAGAAATCAAGAGATTAT 465		
QY	106 SerGlnAlaGlnLysSerProValLysSer-----LysSerThrHisArgIleGln 122		
DB	466 CTGTAAACCCAGACGCGCGGTCAAAAGCAAAACACACACACCCGCCAGACCCGA 525		
QY	123 HisAsnIleAspTyrLeuLysHisLeuSerLysValLysLysIleProSerAspPheGlu 142		
DB	526 CGGAGCATCTACTACCTGACACATCTCCACAGCAAGAGACTCCCACTGACCTTGAA 585		
QY	143 GlySerGlyTyrThrAspLeuGlnArgGlyAspAsnAspIleSerProPheSerGly 162		
DB	586 GGCAGTGGCTCCCAAGATCTTCTAGTGGGAGATTAATGATGTCCTCCCTTTCAGTGA 645		
QY	163 AspGlyGlnProPheLysAspIleProGlyLysGlyGluAla---ThrGlyProAspLeu 181		
DB	646 GATGGCAACATTTTATGCACATTCCTGGCAAGAGAGTGTGGGTCTGTCTCTGAA-- 702		
QY	182 GluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeu 201		
DB	703 -----AGCTCAACTAGTGGCCCCCTCTCAGCTCCAGCAAGCTGAAGTATTGACCCA 756		
QY	202 AspThrLysLysProGlyTyrAsnGluLeuProGluArgGluAsnGlyGlyAsnThr 221		
DB	757 CATATGAGTGACCTAGGCTCTAATGAGATCCCGGAGAGAGACATGTGTGGCAGTGC 816		
QY	222 IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGlu 241		
DB	817 TATGCAACACAGACAAAGCTGCACAGGGGCGAGCTCTGCAGGTGGAGCCTTGTGGGG 876		
QY	242 GlySerAsnAspIleMetGlySerThrAsnPhenLysGluLeuProGlyArgGluGlyAsn 261		
DB	877 GGCAGCATGAATACAGAGCAGACCAATTTTACAGGNACTCCCGGAAGAAGAGGAAC 936		
QY	262 ArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrProPro 281		
DB	937 AGAATTAATGCGGCGGCAAAATGCTCATCAAGGAAAGTAGAATTTTCAATATCCCAA 996		
QY	282 AlaProSerLysGluLysArgLysGluGlySerSerAspAlaAlaGluSerThrAsnTyr 301		
DB	997 GTGGCTCGAGAGAAAGGTAAGGGGCGGTGGAGCATGCGGAGAGCT---GGTTAC 1053		

QY	302	AsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsnArg	321
DB	1054	AACGAAATCCCAAGACGACCAAGGTAGCTCTAGCAAGATGTCAGAAAGTCCCAAGGG	1113
QY	322	AsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGlyLeu	341
DB	1114	AACCAATTAACCTTGACTGCAAGCCAAAGATTTCCTAGGTAAAGGCCAAAGCCAGG	1173
QY	342	ProIleProSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsnGly	361
DB	1174	GCTCTGCCCTCTCACAGTCTTAGTAATAGAGTTAAAGTGA	1215
QY	362	ProSerHisGluAsnIleIleThrHisGlyArgLysTyrHisTyrValProHisArgGln	381
DB	1216	-----GAAAAAC-----CATTATGTTTCCATGGACAA	1242
QY	382	AsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySerTrp---GlyArgGln	400
DB	1243	AATATCTTACACCGAATAAAGGATGTACACGGAGAGGCTCTCGGCTTCGAGAAGA	1302
QY	401	ProHisSerAsnArgArgPheSerSerArgArgArgAspAspSerSerGluSerSerAsp	420
DB	1303	CCCAATTCACACACGGCGGTAGCACCCGCCAAGA--GACAGCAGCGAGTCGTATCC	1359
QY	421	SerGlySerSerSerGluSerAspGlyAsp	430
DB	1360	AGTGGAGTCTTAGTGAGAGTCATGTTGAC	1389
RESULT 8			
US-09-794-422-1			
; Sequence 1, Application US/09794422			
; Publication No. US20030166239A1			
; GENERAL INFORMATION:			
; APPLICANT: Brown, Thomas A.			
; APPLICANT: De Wet, Jeffrey R.			
; APPLICANT: Gowen, Lori C.			
; APPLICANT: Hanes, Lynn M.			
; TITLE OF INVENTION: Mammalian Osteoregulins			
; FILE REFERENCE: PCI0445			
; CURRENT APPLICATION NUMBER: US/09/794,422			
; CURRENT FILING DATE: 2001-02-27			
; PRIOR APPLICATION NUMBER: 60/185,617			
; PRIOR FILING DATE: 2000-02-29			
; PRIOR APPLICATION NUMBER: 60/234,500			
; PRIOR FILING DATE: 2000-09-22			
; NUMBER OF SEQ ID NOS: 46			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 1			
; LENGTH: 1655			
; TYPE: DNA			
; ORGANISM: Rattus norvegicus			
US-09-794-422-1			
Alignment Scores:			
Pred. No.:	2.66e-82	Length:	1655
Score:	938.50	Matches:	211
Percent Similarity:	59.95%	Conservative:	45
Best Local Similarity:	49.41%	Mismatches:	146
Query Match:	41.18%	Indels:	25
DB:	12	Gaps:	8
US-09-700-696C-2 (1-430) x US-09-794-422-1 (1-1655)			
QY	9	AsnLysGluAsnThrHisAsnGlyLeuArgMetSerIleTyrProLysSerThrGlyAsn	28
DB	146	AACCAAGCAACATCCAC-----TTAGCATCTGTGAAGCTGAGCCCATGTGGGT	196
QY	29	LysGlyPheGluAspGlyAspAlaIleSerLysLeuHisAspGlnGluIuTyrGly	48
DB	197	AAAGGAAACAGAGGGTGGCGGAGATGCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTT	256
QY	49	AlaAlaLeuIleArgAsnAsnMetGlnHisIleMetGlyProValThrAlaIleLysLeu	68

RESULT 8

US-09-794-422-1
; Sequence 1, Application US/09794422
; Publication No. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulin
; FILE REFERENCE: PCI0445
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1655
; TYPR: DNA
; ORGANISM: Rattus norvegicus
US-09-794-422-1

Alignment Scores:	
Pred. No.:	2,66e-82
Score:	938.50
Percent Similarity:	59.95%
Best Local Similarity:	49.44%
Query Match:	41.18%
DB:	12
Length:	
Matches:	211
Conservative:	45
Mismatches:	146
Indels:	25
Gaps:	8

US-09-700-696C-2 (1-430) x US-09-794-422-1 (1-1655)

QY	9 AsnLysGluAsnThrHisAsnGlyLeuArgMetSerIleTyrProLysSerThrGlyAsn 28		
DB	146 AACCAAGCAACATCCAC-----TTAGCATCTGTGAAGCCTGAGCCCATGTGGGT 196		
QY	29 LysGlyPheGluAspGlyAspAlaIleSerLysLeuHisAspGlnGluGlyGly 48		
DB	197 AAAGGACAGAGGGTGGGCGAGATGCTCCCTTCACCTGCTTGACCAAGACAGGAGGT 256		
QY	49 AlaAlaLeuIleArgAsnAsnMetGlnHisIleMetGlyProValThrAlaIleLysLeu 68		

Db 257 GCCACCCCTCCCTCAGAAATATCACTCAGCCTGTAAAGAGTCTGGTGACGGGACTGAGTA 316
QY 69 LeuGlyGluGluAsnLysGluAsnThrProArgAsnValLeuAsnIleIleProAlaSer 88
Db 317 CAGACGACAGAAACAAGAGAGAACTCAGAGTGTCTTAAGCGTAATTCACACAGAT 376
QY 89 MetAsnTyrAlaLysAlaHisSerLysAspLysLysProGlnArgAspSerGlnAla 108
Db 377 GTCCACATACTAAGACTACTCAGAGATACAGAGAACCAACAGAGGATCTACTACTC 436
QY 109 GlnLysSerProValLysSerLysThrHisArgIleGlnHisAsnIleAspTyrLeu 128
Db 437 CAGAACCCAGAGCAAGCAACACACCCTCGGCCCGCAGCAAGCAGCAGCTACTACTA 496
QY 129 LysHisLeuSerLysValLysLysIleProSerAspPheGluGlySerGlyTyrThrAsp 148
Db 497 ACACATCTCCCCCAATCAGAAAGATCTCAGTACTTCGAGGACAGTCTCCCGAC 556
QY 149 LeuGlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGlyGlnProPheLys 168
Db 557 CTTCTAGTAGGGGGGATAATGATGTCTCCTCTTTCAGTGGAGATGGCAACATTTATG 616
QY 169 AspileProGlyLysGlyGluAlaThrGlyProAspLeuGlu-----GlyLysasp 185
Db 617 CACACTCCGACAGAGAGGTCTGTGGATCTGATCTGAAAGCTCAGCTGGTCCACCT 676
QY 186 IleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAspThrLysLys 205
Db 677 GTG-----TCAGGCTCCAGCAATGTCAGATGTTGTGACCCACACAGCAATGGA 724
QY 206 ProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsnThrIleGlyThrArg 225
Db 725 CTGGGCTCTAATGATGCCAGGAGAGAGGTACATAGCGGTGCTATGCAACCCAGA 784
QY 226 AspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGluGlySerAsnAsp 245
Db 785 GGAATAACTCGCAGGGGGCAGGTTCGCGATGTGAGCTTGTGGGGCGAGCAATGAA 844
QY 246 IleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGlyAsnArgValAspAla 265
Db 845 ATCAGCGGCGATCCAAATTTAGGAGTCTCCTCGAAAGAGAAAGCAACAGAGTCGATGCC 904
QY 266 GlySerGlnAsnAlaHisGlnGlyValGluPheHisTyrProProAlaProSerLys 285
Db 905 AGACGCCAAATGCTCATCAAGGAAAGATGAATTCCTACCCACAGCGCCCTCAAAA 964
QY 286 GluLysArgLysGluGlySerSerAspAlaAlaGluSerThrAsnTyrAsnGluIlePro 305
Db 965 GAGAAAGTAAAGGGGCGACGAGGAGCACACAGGGAAGCGGTTACATGAAATCCCC 1024
QY 306 LysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsnArgAsnGlnAlaThr 325
Db 1025 AAGAGCAGCAAGGGCGCGCTAGCAAGGATCGCGAAGATCTAAAGGGAACCAAGTAACC 1084
QY 326 LeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGlyLeuProIleProSer 345
Db 1085 TTGACTGAAGCCAAAGTTCCAGGCAAGAGCAAGGCCAGTCT-----TCT 1132
QY 346 ArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsnGlyProSerHisGlu 365
Db 1133 CACAGTCTTGTAATAGGTTAAAGTGAAGAGACTCTTCTAATAGTCTCAGTAGAG 1192
QY 366 AsnIle---IleThrHisGlyArgLysTyrHisTyrValProHisArgGlnAsnAsnSer 384
Db 1193 GGGATTGCAATAGCACAGGAGAACCAAGCCAC-----CCT 1228
QY 385 ThrArgAsnLysGlyMetProGlnGlyLysGlySerTyr---GlyArgGlnProHisSer 403
Db 1229 ACAGGGAATAGGGGATGTTCACAGCGGAGAGGCTCTCTGGCCCTCGAAGACCCCATCC 1288
QY 404 AsnArgPheSerSerArgArgAspAspSerSerGluSerSerAspSerGlySer 423
Db 423

Db 1289 CACCGCGCGTAAGCACCCGCCAAAGA---GACAGTAGTAGTATCATCATCCAGTGGAGT 1345
QY 424 SerSerGluSerAspGlyVasp 430
Db 1346 TCTAGCGAGACGAGTGGTGAC 1366

RESULT 9

US-10-363-798-1
; Sequence 1, Application US/10363798
; Publication No. US20030180280A1
; GENERAL INFORMATION:
; APPLICANT: Kong, Xiangyin
; APPLICANT: Xiao, Shangxi
; APPLICANT: Zhao, Guoping
; APPLICANT: Yu, Chuan
; APPLICANT: Hu, Landian
; TITLE OF INVENTION: METHOD OF DIAGNOSING AND TREATING DENTINOGENESIS IMPERFECTA
; TITLE OF INVENTION: TYPE II USING DENTIN SIALOPHOSPHOPROTEIN GENE AND CODED
; TITLE OF INVENTION: PRODUCT THEREOF
; FILE REFERENCE: 9548.78USWO
; CURRENT APPLICATION NUMBER: US/10/363,798
; PRIOR FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: CN 00125042.6
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 8201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-363-798-1

Alignment Scores:
Pred. No.: 0.000546 Length: 8201
Score: 148.50 Matches: 92
Percent Similarity: 38.43% Conservative: 84
Best Local Similarity: 20.09% Mismatches: 218
Query Match: 6.52% Indels: 64
Gaps: 14

US-09-700-696C-2 (1-430) x US-10-363-798-1 (1-8201)

QY 4 GluTyrSerIleSerAsnLysGluAsnThrHisAsnGlyLeuArgMetSerIleTyrPr 23
Db 5214 AAATATCTACTAGTTAATCATCTTCTCCATCTCTCCATAGGGAATAGAAATCAAGG 5273
QY 23 oLysSerThrGlyAsnLysGlyPhe-----GluAspGlyAspAspAlaIleSerLysLe 41
Db 5274 TCCAGCAGTGGCAACAAATATTACCAAGAAAGTTGGGAAAGGCAACGAAGGTAAA-- 5331
QY 41 uHisAspGlnGluTyrGlyAlaAlaLeuIleArgAsnAsnMetGlnHisIleMetGl 61
Db 5332 -GAGGATAAGGACACATCGAATGATCTTGGCAAGGCAATGTCAAG--ACACAAGG 5387
QY 61 yProValThrAlaIleLysLeuLeuGlyGluGluAsnLysGluAsnThrProArgAsnVa 81
Db 5388 AGAGGTGTCAACATAGAGGACCTGGCCCAAAAATCAGAA-----CCAGGAATAA 5438
QY 81 lLeu-----AsnI 84
Db 5439 AGTGGACACAGCAATACAGGTAGTGACAGCAATAGTGTGATGATGATGATGATTT 5498
QY 84 elleProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLysLysProGlnAr 104
Db 5499 TGATGATAAGTCCATCAAGGAGATGATCCCAATAGCAGTATGATCTTAATGCGCAATGA 5558
QY 104 gAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArgIleGlnHisAs 124
Db 5559 TGATGCTAATTCAGAA---AGTGACAATAACAGCAGTAGCCGAGGAGATGTCTTCTTATAA 5615
QY 124 nIleAspTyrLeuLysHisLeuSerLysValLysLysIleProSerAspPheGluGlySe 144
Db 5616 CTCTGATGAA-----TCAAAAGATAATGGCAATGGCAGTACTCAAAAGGAGC 5663

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QY 144 rGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspG1 164
Db 5664 AGAAGATGATGACAGTATGACATGACATCACTAATAATAGTACAGTAAATGCCAATGG 5723
QY 164 yGlnProPheLysAsp-----IleProGlyLysGlyGluAlaThrGlyPr 179
Db 5724 TAACAATGGGAATGATGACAATGACAAATCAGACAGTGGCCAAAGGTAAATCAGATAGCAG 5783
QY 179 oAspLeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerTh 199
Db 5784 TGACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5843
QY 199 rHisLeuAspThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyG1 219
Db 5844 CAGCAGTATGACAAACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5903
QY 219 yAsnThrIleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLe 239
Db 5904 CAGTGACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5960
QY 239 uValGluGlySerAsnAspIleMetGlySerThrAsnPhelLysGluLeuProGlyArg-- 258
Db 5961 TAGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6020
QY 259 -----GluGlyAsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValG1 276
Db 6021 AGAGACGACAGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6080
QY 276 uPheHisTyrProProAlaProSerLysLysLysArgLysGluGlySerSerAspAla1 296
Db 6081 CAGTAGTGACAAACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6140
QY 296 aGluSerThrAsnTyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyVa 316
Db 6141 TGACAGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6195
QY 316 lAspHisSerAsnArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysG1 336
Db 6196 -GACAGCAGCAACAGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6254
QY 336 yLysSerGlnGlyLeuProIleProSerArgGlyLeuAspAsnGluIleLysAsnGluMe 356
Db 6255 CAGTGATAGT-----AGTGACAGCAGTATGATGATGATGATGATGATGATGATGATG 6299
QY 356 tAspSerPheAsnGlyProSerHisGluAsnIleThrHisGlyArgLysTyrHisTy 376
Db 6300 TGACAGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6330
QY 376 rValProHisArgGlnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySe 396
Db 6331 -----GACAGCAGCAACAGCAGTATGATGATGATGATGATGATGATGATGATGATG 6380
QY 396 rTrpGlyArgGlnProHisSerAsnArgArgPheSerSerArgArgAsp-----413
Db 6381 CAGCAACAGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6440
QY 414 -----AspSerSerGluSerSerAspSerGlySerSerSerGluSerAsp 428
Db 6441 TAGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6492
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RESULT 10

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US-09-785-770A-15
; Sequence 15, Application US/09785770A
; Patent No. US20020103360A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: A NOVEL PROTEIN RELATED TO MELANOMA-INHIBITING PROTEIN
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 07334-328001
; CURRENT APPLICATION NUMBER: US/09/785, 770A
; CURRENT FILING DATE: 2001-02-16
```

```
; PRIOR APPLICATION NUMBER: US 09/387,462
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: US 09/145,056
; PRIOR FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 4.0
; SEQ ID NO 15
; LENGTH: 5721
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)....(5721)
US-09-785-770A-15

Alignment Scores:
Pred. No.: 0.000382 Length: 5721
Score: 148.00 Matches: 106
Percent Similarity: 34.76% Conservatives: 65
Best Local Similarity: 21.54% Mismatches: 209
Query Match: 6.49% Indels: 112
DB: 10 Gaps: 24

US-09-700-696C-2 (1-430) x US-09-785-770A-15 (1-5721)
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QY 1 ValAsnLysGluTyrSerIleSerAsnLys-----GluAsnThrHisAsnGly 16
Db 1372 GTAACGCGCAGAACATCACATTAAGGAAAGGAGGGAGGAGTTCAGGAATCCAGAGGGGC 1431
QY 17 Leu-----ArgMetSerIleTyrPro 23
Db 1432 CTGGTACAGATGAGCAGCAATTAGAGGATGAAATCAAGAGGCATGACTGTGCACAGT 1491
QY 24 LysSerThrGlyAsnLys-----GlyPheGluAspGlyAspAlaIle 38
Db 1492 TCTGTTTCACAGCAATACCTCACTCTATGCCAGCTGCTGAAAGGTTAAGACACATTA 1551
QY 39 SerLysLeuHisAspGlnGlu-----TyrGlyAlaAlaLeu-----IleArgAsn 54
Db 1552 AAATCAGCTTATGATGATACAGAAATGACCTAAAGAGGAGCAGCTATTATCTCAAAA 1611
QY 55 AsnMetGlnHisIleMetGlyProValThrAlaIleLysLeuLeuGlyGluGluAsnLys 74
Db 1612 GGAATGCTCCAGAGAAAGGCTCGAGAGCAGATTTTGGAAAGTGGCTCAGAGAGTGAA 1671
QY 75 -----GluAsnThrProArgAsnValLeuAsn-----IleIleProAlaSerMet 89
Db 1672 TCTGCACAGAAAGCTGCAGGGAATCAATGAATGACAGAAAGATTCAACAGGAATCCTG 1731
QY 90 AsnTyrAlaLysAlaHisSerLysAspLysLysLysProGlnArgAspSerGlnAlaGln 109
Db 1732 GGTAGTGACCACTCATGCGAGATGACCACTTAACGCATCCAGACAGAGTGTGGAGGA 1791
QY 110 LysSerProValLysSerLysSerThrHis-----ArgIleGlnHisAsnIleAspTyr 127
Db 1792 GACGCTTGGTAAATGGGGCCAAACTGCACACGCTTTTCAGTGGAGCATCAACGTGAGGA 1851
QY 128 LeuLysHis-----LeuSerLysValLysLysIleProSerAspPheGluGlySerGly 145
Db 1852 TTGAAAGAGGAATTAGTTCTTAAACTCAAAACCAACCTAGA---TTCTCTCTCCAGAT 1908
QY 146 TyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGlyGln 165
Db 1909 GAGATTGATTATGCCAGAGAACTGGAAGACGAGGTT---CCCATTTCTGGAGAAATCTT 1965
QY 166 ProPhe-----LysAspIleProGlyLysGlyGluAlaThrGlyProAspLeuGlu 182
Db 1966 CCTCGCACCAAGAAAGAGATGTG-----GCTGCCACAGCCAGTAAAGCAAAATG 2013
QY 183 GlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAsp 202
Db 2014 AGTGAGAGATAGG-----CTCTCTGAGGAGAGCAAGCAAGAGAGCTCTCTGGAT 2064
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QY 203 ThrLysLysProGlyTyrAsnGluLeuProGluArgGluGluAsnGlyGlyAsnThrIle 222
Db 2065 -----GAAGAGT-----CATCAAGGCAATCGAGGGCAGACAGAGTA 2106
QY 223 GlyThrArgAspGluThr-----AlaLysGlu 231
Db 2107 GGACAGACAGACCAAACTGACACGACAGGAGGACCAGCTTCCCTTCTAAAGTAGAGAG 2166
QY 232 AlaAspAlaValSerLeuValGluGlySerAsnAspIleMetGlySerThrAsn 251
Db 2167 GATGATTATCCCTCTGAAGAACTACTAGAGATGAAACCGTATAAATGCAAAACGGTCT 2226
QY 252 PheLysGluLeuProGlyArgGlyAsnArgValAspAlaGlySerGln----- 268
Db 2227 AAGAAAAAACCCGGGAATCAGCGGAGGAGGAGTGTGATGTAATCTCAAGTCCCTGAC 2286
QY 269 AsnAlaHisGlnGlyLysValGluPheHisTyrProProAlaProSerLysGluLysArg 288
Db 2287 AGAGCAGTGTAGGACCAATTCAT-----CCAGATCCAGAAATTTGAAGAAAGC 2334
QY 289 LysGluGlySerSerAspAlaAlaGluSerThrAsnTyrAsnGluLeuProLysAsnGly 308
Db 2335 AAGCAAGAACTAGTATGATTTTGGATAGTGAATAAACAAGTGAG----- 2379
QY 309 LysGlySerThrArgLysGlyValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGlu 328
Db 2380 -----ACTGCTGCCAAGGGGTCAACACAGGAGCGAGGAAACCAAGTGAG----- 2433
QY 329 LysGlnArg-----PheProSerLysGlyLysSer 338
Db 2434 AAAGACGCCCTTGGCAGATAGAAAGACACAGAGACCATTTGAACGAAGTGACTTTCT 2493
QY 339 GlnGlyLeuProLysProSerArgGlyLeuAspAsnGluLeuLysAsnGluMetAspSer 358
Db 2494 GACAGCAATAAAATCAGACTCCAGAAATAGGTGAAGTGTTCAGAAATAAGATTCGTAT 2553
QY 359 Phe-----AsnGlyProSerHisGluAsnIleThrHisGlyArgLysTyrHisTyr 376
Db 2554 TATCTGAAGAACGACCAACCTCGAGGAACATCTGAAGACCTCAGGCGTT----- 2601
QY 377 ValProHisArgGlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySer 396
Db 2602 -----GCAGGGAGCGCTGAGGAGAACTCTCA 2628
QY 397 TrpGlyArgGlnProHisSerAsnArgArgPheSerSerArgArgArgAspAspSerSer 416
Db 2629 -----AAAGAGACCAATGAGAAC-----ACAGAGAAAGTACATGGGCACA 2667
QY 417 GluSerSerAspSerGlySerSerSerGluSerAsp 428
Db 2668 GAAAGCCAGGGGTCTGCTGCTGCAGAACCTGAAGAT 2703
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RESULT 11

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US-09-785-770A-14
; Sequence 14, Application US/09785770A
; Patent No. US20020103360A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; APPLICANT: Barnes, Thomas M.
; TITLE OF INVENTION: A NOVEL PROTEIN RELATED TO MELANOMA-INHIBITING PROTEIN
; FILE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 07334-328001
; CURRENT APPLICATION NUMBER: US/09/785,770A
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/387,462
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: US 09/145,056
; PRIOR FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 4.0
; SEQ ID NO 14
; LENGTH: 8121
; TYPE: DNA
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)...(4)
; NAME/KEY: CDS
; LOCATION: (5)...(5725)
; NAME/KEY: 3'UTR
; LOCATION: (5726)...(8121)
US-09-785-770A-14
Alignment Scores:
Pred. No.: 0.000603 Length: 8121
Score: 148.00 Matches: 106
Percent Similarity: 34.76% Conservative: 65
Best Local Similarity: 21.54% Mismatches: 209
Query Match: 6.49% Indels: 112
DB: 10 Gaps: 24
US-09-700-696C-2 (1-430) x US-09-785-770A-14 (1-8121)
QY 1 ValAsnLysGluTyrSerIleSerAsnLys-----GluAsnThrHisAsnGly 16
Db 1376 GTHAACGACGACATCACATTAAAGGAAAGGGAGGGAGTTCAGGATCCAAAGGGGC 1435
QY 17 Leu-----ArgMetSerIleTyrPro 23
Db 1436 CTGGTACAGATGAGACAGAAATTAGAGATCAAAATCAAGAAGGCATGACTGTGCACAGT 1495
QY 24 LysSerThrGlyAsnLys-----GlyPheGluAspGlyAspAspAlaIle 38
Db 1496 TCTGTTTACAGCAATAACCTCAACTCTATGCCAGCTCTGTAAGAGGGTAAAGACACATTA 1555
QY 39 SerLysLeuHisAspGlnGlu-----TyrGlyAlaAlaLeu-----IleArgAsn 54
Db 1556 AAATCAGCTTATGATGATACAGAAATGACCTAAAGAGGAGCAGCTATTCTATCTCAAAA 1615
QY 55 AsnMetGlnHisIleMetGlyProValThrAlaIleLysLeuLeuGlyGluAsnLys 74
Db 1616 GGAATGCTCCACGAAAGAAAGCCCTGGAGAGCAGATTTTGAAGGTGCTCAGAGAGTGA 1675
QY 75 -----GluAsnThrProArgAsnValLeuAsn-----IleIleProAlaSerMet 89
Db 1676 TCTGCACAGAAAGCTGAGGGAATCAATGAATGACAGAAAGATTCAACAGGAATCCCTG 1735
QY 90 AsnThrAlaLysAlaHisSerLysAspLysLysLysProGlnArgAspSerGlnAlaGln 109
Db 1736 GGTAGTGACCACTCTGAGGAGATGACCACCTAACGCATCCACAGACAGTGTGGAGGA 1795
QY 110 LysSerProValLysSerLysSerThrHis-----ArgIleGlnHisAsnIleAspTyr 127
Db 1796 GACGCTTTGGTAAATGGGGCCAAACTGCACACGCTTTTCAGTGGAGCATCAACGTGAGAA 1855
QY 128 LeuLysHis-----LeuSerLysValLysLysLysLysProSerAspPheGluGlySerGly 145
Db 1856 TTGAAGAGGAATAGTCTTAAACTCAAAACCAACTAGA---TTCTCCTCTCCAGAT 1912
QY 146 TyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGlyGln 165
Db 1913 GAGATTGATTGGCCAGAGAACTGGAAGACAGAGTT---CCCATTCTGGGAGAAATCTTT 1969
QY 166 ProPhe-----LysAspIleProGlyLysGlyGluAlaThrGlyProAspLeuGlu 182
Db 1970 CCTGGCAACAAGAAAGAGATGTG-----GCTGCCACGCCAGTAAGCAAAATG 2017
QY 183 GlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAsp 202
Db 2018 AGTGAGAGATTAAG-----CTCTCTGAGGAGAGCAACCAAGAGGAGCTCTCTGGAT 2068
QY 203 ThrLysLysProGlyTyrAsnGluLeuProGluArgGluGluAsnGlyGlyAsnThrIle 222
Db 2069 -----GAAGAGT-----CATCAAGGCAATCGAGGGCAGACAGAGTA 2110
QY 223 GlyThrArgAspGluThr-----AlaLysGlu 231
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Db      2111  GGACAGACAGACCAAACTGACAGACAGGAGCCAGCTTCTCTTCTTAAAGTAGAGAG 2170
QY      232  AlaAspAlaValAspValSerLeuValGluGlySerAsnAspMetGlySerThrAsn 251
Db      2171  GATGATTATCTCTGTAAGAACTACTAGAGGATGAAACGCTATAAATGCAAAACGGTCT 2230
QY      252  PheGlyLeuProGlyArgGlyAsnArgValAspAlaGlySerGln----- 268
Db      2231  AAGAAAAAACCCGGGAATCAGGCGAGCTTGTATGTTAATCTGCAAGTCCCTGAC 2290
QY      269  AsnAlaHisGlnGlyValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGlu 288
Db      2291  AGAGCAGTTTATAGGACCAATCAT-----CCAGATCCAGAAATTGAGAAAGC 2338
QY      289  LysGluGlySerSerAspAlaAlaGluSerThrAsnTyrAsnGluLeuProLysAsnGly 308
Db      2339  AAGCAAGAACTAGTATGATTTGGTAGTGAAGAAACAAAGTGAG----- 2383
QY      309  LysGlySerThrArgLysGlyValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGlu 328
Db      2384  -----ACTGCTCCAAAGGGTCAACACAGGAGCGAGGAACCAATACAAATGTTGGAA 2437
QY      329  LysGlnArg-----PheProSerLysGlyLysSer 338
Db      2438  AAGAAGCGCCTCTGCGAGATAAGAAAGCACAGAGACCAATTTGAACGAGTGACTTTCT 2497
QY      339  GlnGlyLeuProLysProSerArgGlyLeuAspAsnGluLeuLysAsnGluMetAspSer 358
Db      2498  GACAGCATAAATTCAGACTCCAGATTAAGTGAAGTGTTCAGAAATAAGATTCTGAT 2557
QY      359  Phe-----AsnGlyProSerHisGluAsnLeuLeuThrHisGlyArgLysTyrHisTyr 376
Db      2558  TATCTGAAGAACACACACCTGAGGACATCTGAGACCTCAGACCTCAGGGCTT----- 2605
QY      377  ValProHisArgGlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySer 396
Db      2606  -----GCAGGGGAGCCTCAGGAGAACTCTCA 2632
QY      397  TrpGlyArgGlnProHisSerAsnArgArgPheSerSerArgArgAspAspSerSer 416
Db      2633  -----AAGAGGACCATGAGAAC-----ACAGAGAAGTACATGCGGCACA 2671
QY      417  GluSerSerAspSerGlySerSerSerGluSerAsp 428
Db      2672  GAAAGCCAGGGGTCTGCTGCTGCGAGAACCTGAAGAT 2707

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RESULT 12

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US-10-153-668-301
; Sequence 301, Application US/10153668
; Publication No. US20030092616A1
; GENERAL INFORMATION:
; APPLICANT: HONDA, Goichi
; APPLICANT: MATSUDA, Akio
; APPLICANT: MURAMATSU, Shuji
; APPLICANT: ISHIZAWA, Kenya
; TITLE OF INVENTION: STAT6 Activating Gene
; FILE REFERENCE: 1254-0207P
; CURRENT APPLICATION NUMBER: US/10/153,668
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/293,172
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/316,031
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/328,403
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: JP 2001-157043
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: JP 2001-260681
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: JP 2001-313175
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 488

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 301
; LENGTH: 2673
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (33)..(2348)
US-10-153-668-301

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Alignment Scores:

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Pred. No.: 0.00062 Length: 2673
Score: 140.00 Matches: 87
Percent Similarity: 32.08% Conservative: 49
Best Local Similarity: 20.52% Mismatches: 144
Query Match: 6.14% Indels: 144
DB: 14 Gaps: 17

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US-09-700-696C-2 (1-430) x US-10-153-668-301 (1-2673)

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QY      23  ProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAspAlaIleSerLysLeuHis 42
Db      660  CCTGGGAAAGGCCACAGCAATGCTTTTCAGACAGACTCGGGGCCAGCCAGACGACAC 719
QY      43  AspGlnGluGluTyrGlyAlaAlaLeuLeuArgAsnAsnMetGlnHisIleMetGlyPro 62
Db      720  CTGGGTGAACCCCATCGGAAAGGGTTGTGAGTCAAAACAAGAGGACAC----- 767
QY      63  ValThrAlaIleLysLeuLeuGlyGluGluAsnLysGluAsnThrProArgAsnValLeu 82
Db      767  ----- 767
QY      83  AsnIleProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLysLysPro 102
Db      768  -----AAATCTCCCAAGAGCAAAACGCCCGTG 797
QY      103  GlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArgIleGln 122
Db      798  GATGCCAAGAGTGATGAGAAGGCTCTGTGTGTCAGCAGAGAGAAATCACAC----- 848
QY      123  HisAsnIleAspTyrLeuLysHisLeuSerLysValLysLysLysLysLysLysLys 142
Db      849  -----AAGGCCCTCTCCAAA----- 863
QY      143  GlySerGlyTyrThrAspLeuGlnGluArgLysAspAsnAspLysSerProPheSerGly 162
Db      864  -----GAGGAGAACCGAGGCCACCTCAGG 890
QY      163  AspGlyGlnProPheLysAspLysProGlyLysGlyGluAlaThrGlyProAspLeuGlu 182
Db      891  GACAAATGCAAGGAGAGAAACCG---CCCTCTAGTGGGTAAAGAAAGAGAGAGAGAGAG 947
QY      183  GlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSer---ThrHisLeu 201
Db      948  GGCAGCAGCTGAAGAGAGAGTGTTCCTCCTCAGAGCGCTTCAGAACCCACCTG 1007
QY      202  AspThrLysLysProGlyTyrAsnGluLeuProGluArgGluGluAsnGlyGlyAsnThr 221
Db      1008  -----AAAAAGCCAAAGCACAGAGAC---CCAGAGAAAGCCCAA----- 1043
QY      222  IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGlu 241
Db      1044  -----TTGGACAAAAGCAAGCAAGTCTGAGACAGCTTTGACACAGGA-----AAA 1088
QY      242  GlySerAsnAspIleMet-----GlySerThrAsnPheLysGluLeu 255
Db      1089  GGAGCAGAGAGCTTGTGCCCAAGGTAAAGAGAGAGGGTTCCTAAACACTAAGACTCCA 1148
QY      256  ProGlyArgGluGlyAsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysVal 275
Db      1149  GAAAGGAAAGTCAAAACCTAATTGTGATAGAAAGTCACTGGGGCTCC---CTCCCTAAAGTT 1205
QY      276  -----GluPheHisTyrPro----- 280

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Db 1206 GAGGAGACAGATATGAGGATGAATTCAGACAGCCAAACCATGTCTTTTGAATCTCTACCTC 1265
Qy 281 -----ProAlaProSerLysGluLysArgLysGluGlySerSerAspAlaAlaGluSer 298
Db 1266 AGCTATGACACAGCCCGGAGAGAAAAGAAAGATTGTGAAACT---TCAGCCACGGCA 1322
Qy 299 ThrAsnTyrAsnGluLysProLysAsnGlyLysGlySerThrArgLysGlyValAspHis 318
Db 1323 CTTGGAGATAAAGACTTAAATAAAATGACTCTTAAAGCACTGTGTAATAAACTTGCACTCA 1382
Qy 319 SerAsnArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSer 338
Db 1383 GTTCAGAAATTACCAAGGTGAACAAACCAAGTCAGAGAGCCCGCTGGAGCTGATTTA 1442
Qy 339 GlnGlyLeu----- 341
Db 1443 GCCAAGCTGAGAAAGTGCTGATGTGTGCCAGTGTTCAGACCTCCCGTTTACCCGCG 1502
Qy 342 -----ProIleProSerArgGlyLeuAspAsnGluLysLeuAsnGlu 355
Db 1503 ATACAGCCCAATTACCGTCCACTCCCTCCCTCGAGCTGATATCCTCCTCCAGCCAAAG 1562
Qy 356 MetAspSerPheAsnGlyProSerHisGluAsn----- 366
Db 1563 CGAAAGCGTCTCTTCAACCCCGAGAGAGAGAGAGAGCTGGATTTACTGGCGCAGAAATG 1622
Qy 367 -----IleIleThrHisGlyArgLysTyrHisTyrValPro----- 378
Db 1623 AATTCCAAGATGACGAGTGTATCTCTGGTTCCAAAGTGTGCTATCTCCCTAAATATGATGACC 1682
Qy 379 ---HisArgGln 381
Db 1683 TTGCACACAGCAA 1694
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RESULT 13

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US-10-101-510-398
; Sequence 398, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 398
; LENGTH: 4839
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (3080)..(3102)
; OTHER INFORMATION: a, t, c, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (4828)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-101-510-398
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Alignment Scores:

Pred. No.:	0.00187	Length:	4839
Score:	140.00	Matches:	87
Percent Similarity:	32.08%	Conservative:	49
Best Local Similarity:	20.52%	Mismatches:	144
Query Match:	6.14%	Indels:	144
DB:	12	Gaps:	17

US-09-700-696C-2 (1-430) x US-10-101-510-398 (1-4839)

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Qy 23 ProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerLysLeuHis 42
Db 663 CTTGGGAAAGGCCACAGCAATGCTTTTCAGCAGACAGCTCGGGGCCAGCAAGAACGACAC 722
Qy 43 AspGlnGluGluTyrGlyAlaAlaLeuIleArgAsnAsnMetGlnHisIleMetGlyPro 62
Db 723 CTGGGTGAACCCCATGGGAAAGGGGTTGTGAGTCAAAACCAAGAGCAC----- 770
Qy 63 ValThrAlaIleLysLeuGluLysGluAsnLysGluAsnThrProAsnValLeu 82
Db 770 ----- 770
Qy 83 AsnIleIleProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLysLysPro 102
Db 771 -----AATCTTCCCAAGGACAAACGCCCGCTG 800
Qy 103 GlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArgIleGln 122
Db 801 GATGCCAAGAGTGATGAGAAAGGCTCTGTGTGAGCAGAGAGAAATCACAC----- 851
Qy 123 HisAsnIleAspTyrLeuLysHisLeuSerLysValLysLysIleProSerAspPheGlu 142
Db 852 -----AAGGCCCTCTCCAA----- 866
Qy 143 GlySerGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspLysSerProPheSerGly 162
Db 867 -----GAGGAGAACCGAGGCCACCTCAGG 893
Qy 163 AspGlyGlnProPheLysAspIleProGlyLysGlyGluAlaThrGlyProAspLeuGlu 182
Db 894 GACAATGCAAGGGAGAGAAACCG---CCCTCTAGTGGGTAAAGAAAGAGAGAGCAGAGAG 950
Qy 183 GlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSer---ThrHisLeu 201
Db 951 GGCAGCAGCTGAGAGAGAGTGTTCCTCTCCCTCAGAGCCGCTTCAGACACACCACCTG 1010
Qy 202 AspThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsnThr 221
Db 1011 -----AAAAAGCCAAAGCACAGAGAC---CCAGAGAAAGCCCAA----- 1046
Qy 222 IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGlu 241
Db 1047 -----TTGACAAAGCAAGCAAGAGTCTGACAGCTTTTCACACAGA-----AAA 1091
Qy 242 GlySerAsnAspIleMet-----GlySerThrAsnPheLysGluLeu 255
Db 1092 GGAGCAGAGAGACTGTTCGCCAAGGTAAAGAGAGAGGTTCTAACACCTTAAGACTCCA 1151
Qy 256 ProGlyArgGluGlyAsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysVal 275
Db 1152 GAAGGGAAAGTCAAAACTAATTGTGGATAGAAAGTCACTGGGCTCC---CTCCCTAAAGTT 1208
Qy 276 -----GluPheHisTyrPro----- 280
Db 1209 GAGGACAGATATGAGGATGAATTCGAGACGCCCAACCATGTCTTTGAATCCTACCTC 1268
Qy 281 -----ProAlaProSerLysGluLysArgLysGluGlySerSerAspAlaAlaGluSer 298
Db 1269 AGCTATGACACCGCCCGGAGAGAAAAGAAAGATTGTGAAACT---TCAGCCACGGCA 1325
Qy 299 ThrAsnTyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHis 318
Db 1326 CTTGGAGATAAAGGACTTAAATAAAATGACTCTTAAAGCACTGGTAAAAAATCTGGACTCA 1385
Qy 319 SerAsnArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSer 338
Db 1386 GTTCAGAAATTACCAAGGTGAACAAACCAAGTCAGAGAGCCCGCTGGAGCTGATTTA 1445
Qy 339 GlnGlyLeu----- 341
Db 1446 GCCAAGCTGAGAAAGGTGCTGATGTGTGCCAGTGTTCAGACCTCCCGTTACCCGCG 1505
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QY 342 -----ProIleProSerArgGlyLeuAspAsnGluIleLysAsnGlu 355
Db 1506 ATACAGGCCAATTAACCTGCTCCCTCCCTGAGCTGATATCTCTTCCAGCCAAAG 1565
QY 356 MetAspSerPheAsnGlyProSerHisGluAsn----- 366
Db 1566 CGAAAAGCGTCTCTTCCACCCAGGAAGAAGAAAGCTGGATTACTGGCGCAGAAATG 1625
QY 367 -----lleIleThrHisGlyArgLysTyrHisTyrValPro----- 378
Db 1626 AATTCCAAAGTGCAGGTGTTATCTGGTTCCAAAGTGTGCTATCTCTCCCTAAATGATGACC 1685
QY 379 ---HisArgGln 381
Db 1686 TTGCACCAGCAA 1697

RESULT 14
US-10-161-572-6
; Sequence 6, Application US/10161572
; Publication No. US20030087266A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: IGS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-097C-PC
; CURRENT APPLICATION NUMBER: US/10/161,572
; CURRENT FILING DATE: 2002-06-03
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 35465
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-161-572-6

Alignment Scores:
Pred. No.: 0.0314 Length: 35465
Score: 139.00 Matches: 105
Percent Similarity: 37.87% Conservative: 48
Best Local Similarity: 25.99% Mismatches: 162
Query Match: 6.10% Indels: 93
DB: 14 Gaps: 17

US-09-700-696C-2 (1-430) x US-10-161-572-6 (1-35465)

QY 74 LysGluAsnThrProArgAsnValLeuAsnIleIleProAlaSerMetAsnTyrAlaLys 93
Db 881 AAACCAAGCAGCATCCCGTAACTCAGTC---ATGAGCCCAAGCAGTTCCTCCAGTCCACAAA 937
QY 94 AlaHisSerLysAspLysLysProGlnArgAspSerGlnAlaGlnLysSerProVal 113
Db 938 TCGACCAAGTACAAAAGAGCCCTTCTTAACCGCCAGCAGCAGGTCCTCCG-AGTCCGCAG 996
QY 114 LysSerLysSerThrHisArgIleGlnHisAsnIleAspTyrLeuLysHisLeuSerLys 133
Db 997 CAAAGCAAGAACACCCAGCAGGCGGTGAGCAC-----CGACACAGGACCCAG 1041
QY 134 ValLysLysIleProSerAspPheGluGlySerGlyTyrThrAspLeuGlnArgGly 153
Db 1042 -----CAAAGCCAGCAGGCCAG 1059
QY 154 AspAsnAspIleSerProPheSerGlyAspGlyGlnProPheLysAspIleProGlyLys 173
Db 1060 CGACGTGATGATCCACCGAGGAGGGGCACACACAGCCGGGTAGGACACCTG-GCAGAA 1118

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QY 174 GlyGluAla-----ThrGlyProAspLeuGluGlyLysAspIle 186
Db 1119 GGGGAAGCCGAGCTTCCAAGAGGTCAACCAGCAGGCGCAGCACTCT-GGCAGG---ATA 1174
QY 187 GlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAspThr----- 203
Db 1175 AGAACTCATGGTGCACAGCAGGATGGCCAGCAGGCGGTGAGAACTCCCACTTCACAGCAA 1234
QY 204 -----LysLysProGlyTyrAsnGluIleProGluArgGluGluAsn--- 217
Db 1235 AAAGGGAGCCGGGAAGAGTTACGGCGCGCTAGAACCCAGCACAGGAAGAGGTGAC 1294
QY 218 -----GlyGlyAsnThrIleGly 223
Db 1295 AGCCAGCCTAGAAATCTGAGCAAGAGAGTTACCGCCCAACCAGGAGGCTCAGGTATAGG 1354
QY 224 ThrArgAspGlu-----ThrAlaLysGluAlaAspAlaValAspVal 237
Db 1355 AGGAGTTCGAGCTGGCTGTAACTCCAGTAGTACAGCCCAAGTGTCAAACCCCGACTGGAATT 1414
QY 238 SerLeuValGluGlySerAsnAspIleMetGlySerThrAsnPheLysGlu----- 254
Db 1415 CCTCCAGGAGGAGAGAGTGCACACCCATCTCCATCTCATCAGGAAGAGTGAAGAGTAC 1474
QY 255 -----LeuProGlyArgGlu-----GlyAsnArg 262
Db 1475 GGTCAAGATGATCATCCCGAGTAGGAAAGAGTTACAGCCCCACTGAAATGTCCAGCAGG 1534
QY 263 ValAspAlaGlySerGlnAsnAlaHisGlnGlyValGluPheHisTyrProPro--- 281
Db 1535 GTCAAGAGTTATAACCAAGCCAGCAGCCCGCAGCAGCGCCGCAAAAGTCAAG-CCAATCTAG 1593
QY 282 AlaProSerLysGluLysArgLysGluGlySerSerAspAla-----AlaGluSerThr 299
Db 1594 AAGCCCCAGAGAGTTCAGAGAGTGGCAGTCAAGAGAGACCAACAGCAGAGTGAAGAGTCA 1653
QY 300 AsnTyrAsnGluIleProLysAsnGlyLysGlySer-ThrArgLysGlyValAspHis 319
Db 1654 CAGTTGGAGAGAAACCATAGCAGGCGCAAGAGTGCACCCCGGAAGGGAATT----- 1705
QY 319 rAsnArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerG 339
Db 1706 ----CTGAGCCAGATGGGAAGACACAGCCAGTCTAGAAGCCACAGCAAGCGGAAAGTCA 1761
QY 339 nGlyLeuPro---IleProSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSe 358
Db 1762 AAACCAATCTAGAACCCCGCAGAAAGAGAGAAAGTCAACTGGTCT----- 1807
QY 358 rPheAsnGlyProSerHisGluAsnIleIleThrHisGlyArgLysTyrHisTyrVal-- 377
Db 1808 ----AGAAACCCAGCAAGGAAGAAAGTCTATAGTCTCCAGAGCTCCAGCAAGAGAG 1863
QY 378 -ProHisArgGlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySerTr 397
Db 1864 AGATCAAGGGGATCTAGCAGCCCGCCAGGAGGAGTGGTTCGAGTCAATCAGGAAGCCC 1923
QY 397 pGlyArgGln---ProHisSerAsnArgPheSerSerArgArgAspAspSerSe 416
Db 1924 CAAACAGCAGAGAGATCACAGCGATCTTAGAAGTCCCAACAGCGCAGAGATCGCAGCG 1983
QY 416 rGluSerSer 419
Db 1984 ATCTAGAACT 1993

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RESULT 15

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US-10-161-572-8
; Sequence 8, Application US/10161572
; Publication No. US20030087266A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: IGS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-097C-PC

```

; CURRENT APPLICATION NUMBER: US/10/161.572

; CURRENT FILING DATE: 2002-06-03

; PRIOR APPLICATION NUMBER: US 60/296,076

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: US 60/328,605

; PRIOR FILING DATE: 2001-10-10

; PRIOR APPLICATION NUMBER: US 60/338,733

; PRIOR FILING DATE: 2001-10-22

; PRIOR APPLICATION NUMBER: US 60/357,253

; PRIOR FILING DATE: 2002-02-15

; PRIOR APPLICATION NUMBER: US 60/357,600

; PRIOR FILING DATE: 2002-02-15

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8

; LENGTH: 36991

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-161-572-8

Alignment Scores:

Pred. No.:	0.0332	Length:	36991
Score:	139.00	Matches:	105
Percent Similarity:	37.87%	Conservative:	48
Best Local Similarity:	25.99%	Mismatches:	162
Query Match:	6.10%	Indels:	93
DB:	14	Gaps:	17

US-09-700-696c-2 (1-430) x US-10-161-572-8 (1-36991)

QY	74	LysGluAsnThrProArgAsnValLeuAsnIlelleProAlaSerMetAsnTyrAlaLys	93
DB	881	AAACAGCGACATCCCGTAACCTGATC---ATGAGCCCAAGCAGTTCAGATCCACCAAA	937
QY	94	AlaHisSerLysAspLysLysProGlnArgAspSerGlnAlaGlnLysSerProVal	113
DB	938	TGACACAGTACAAAGAGCCCTTCTAAACCGGCCAGCAGCAGGTCCCG-AGTCCGAG	996
QY	114	LysSerLysSerThrHisArgIleGlnHisAsnIleAspTyrLeuLysHisLeuSerLys	133
DB	997	CAAGCAAGAACACACAGCAGCGGGGTGAGCAC-----CGACACAGGAGCCAG	1041
QY	134	VallysLysIleProSerAspPheGluGlySerGlyTyrThrAspLeuGlnGluArgGly	153
DB	1042	-----CAAAGCCAGCAGGCCAG	1059
QY	154	AspAsnAspIleSerProPheSerGlyAspGlyGlnProPheLysAspIleProGlyLys	173
DB	1060	CGACCTGAGATGCCACACAGCGAGGGGCACACAGCCGGGGTAGGACACACCTG-CCAGAA	1118
QY	174	GlyGluAla-----ThrGlyProAspLeuGluGlyLysAspIle	186
DB	1119	GGGGAAGCCGAGCTCCAGAGGTCCACAGCGAGGGCCAGCAGCTCT-GGCAGG---ATA	1174
QY	187	GlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAspThr-----	203
DB	1175	AGAACTCATGTGTCAGACAGGATGCCAGCAGCGGGCCAGCAGCTCT-CCACCTTCACAGAA	1234
QY	204	-----LysLysProGlyTyrAsnGluIleProGluArgGluAsn---	217
DB	1235	AAAGGAGCGCGGGGAAGAGTACCGCGCGCTAGAACACAGCAACAGGGGAAGAGGTGAC	1294
QY	218	-----GlyGlyAsnThrIleGly	223
DB	1295	AGCCAGCTTAGAAATCTGAGCAAGAAGATTACCGCCCAACAGGAGGGCTCAGGTATAGGG	1354
QY	224	ThrArgAspGlu-----ThrAlaLysGluAlaAspAlaValAspVal	237
DB	1355	AGGAGTTCGAGCTGGCTGTACTCCAGTACAGCCAAAGTGTCAAAACCCCGACTGGAATT	1414
QY	238	SerLeuValGluGlySerAsnAspIleMetGlySerThrAsnPheLysGlu-----	254
DB	1415	CCCTCAAGGAGAGAGTGAACACCATCTCCATCTCATCAAGGAGGTGAAGAGCTAC	1474

Search completed: November 30, 2003, 02:24:21

Job time : 460 secs

QY	255	-----LeuProGlyVargdu-----GlyAsnArg	262
DB	1475	GTCAGATGATCATCCACAGTAGGAAAGAGATTACAGCCCACTGAAATGTCAGCAGG	1534
QY	263	ValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrProPro---	281
DB	1535	GTCAAGAGTTATAACAGCCAGCAGCCCGCAGCAGCGCAAGTCAAG-CCAATCTAG	1593
QY	282	AlaProSerLysGluLysArgLysGluGlySerSerAspAla-----AlaGluSerThr	299
DB	1594	AAAGCCCAAGAGGTCAAGAAAGTGGCAGTCAGAAAGAGGAGCCACAGCAGTGAAGTCA	1653
QY	300	AsnTyrAsnGluIleProLysAsnGlyLysGlySer-ThrArgLysGlyValAspHisSe	319
DB	1654	CAGTTGGAAGAGAAACCATAGCAGCGCAAGAGTCCACCCCGAAGGGAATT-----	1705
QY	319	rAsnArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerCl	339
DB	1706	----CTGAGCCAGATGGGAAGACACAGCCAGTCTTGAAGCCACAGCAAGGGGAAAGTCA	1761
QY	339	nGlyLeuPro---IleProSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSe	358
DB	1762	AAACCAATCTAGAACCCCAAGAGAGAGAGTCACTGCT-----	1807
QY	358	rPheAsnGlyProSerHisGluAsnIlelleThrHisGlyArgLysTyrHisTyrVal---	377
DB	1808	----AGAAACCCCAAGCAAGAAAGTCAATAGCCATTCCAGAAAGCTCCAGCAAGAGAG	1863
QY	378	-ProHisArgGlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySerTr	397
DB	1864	AGATCAAGGGGATCTAGCGCCCAAGAGAGAGTGTGTCAGTCAATCAGGAGCC	1923
QY	397	pGlyArgGln---ProHisSerAsnArgPheSerSerArgArgAspAspSerSe	416
DB	1924	CAACAGCAGAGAGATCACAGCCGATCTAGAAGTCCCAACAGGCGAGAGATCGCAGCG	1983
QY	416	rGluSerSer	419
DB	1984	ATCTAGAAGT	1993